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OQ9nrs4 sacillus su
Q9kpb2 vibrio chol
p57805 pasteurella
Q9ka05 bacillus ha
P13983 nicotiana t
P579805 pasteurella
Q9ka05 bacillus ha
P13983 nicotiana t
P57346 buchnera ap
Q9chd0 lactococcus
P05797 escherichia
P49750 homo sapien
Q9fp96 chlamydomon
Q9fp96 salmonella
P4368 synechocyst
Q9zbq7 streptomyce
Q51648 borrelia buv
P56118 helicobacte
Q95104 homo sapien
Q53844 spiroplasma
P44441 haemophilus
Q9zhp7 sattus norv
P56118 helicobacte
Q95104 homo sapien
Q53846 borrelia buv
Q53627 rattus norv
P56118 helicobacte
Q95104 homo sapien
Q53846 priroplasma
P4441 haemophilus
Q9zhp7 helicobacte
Q9xcy pseudomonas
P4258 rattus norv
Q9xcy pseudomonas
Q9xb97 chlamydia m
P51532 homo sapien
P12978 epstein bar
Q9z9c7 chlamydia p
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45	44	43	42	41	40	39	38	37	36	35	34
218	218	218	220.5	221	222	222.5	223	223.5	223.5	225	225.5
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		P06599 daucus caro								084299 chlamydia t	Q9ze31 rickettsia

ALIGNMENTS

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-i- SUBURIT: Interacts with Spli- SUBURIT: Interacts with Spli- SUBCELLULAR LOCATION: Nuclear. A fraction is translocated to the nucleolus during the S phase of the cell cyclei- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be produced by alternative splicingi- TISSUE SPECIFICITY: Ubiquitousi- SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN.	SEQUENCE OF 706-1374 FROM N.A. TISSUE-ADOTA: Wei Y.J., Ding J.F., Xiong H., Zhou Y., Liew C.C.; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases. -i- FUNCTION: Involved in pre-rRNA processing. Cleaves double-strand RNA and does not cleave single-strand RNA. -i- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'- -phosphomonocaster.	SEQUENCE OF 603-1374 FROM N.A. TISSUE-Embryo; ISOgai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Nishikawa T., Nagai K., Sugano S., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Takanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yihomiya K., Iwayanagi T.; "NEDO human cDNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.	SEQUENCE FROM N.A. (ISOFORM 1). MEDLINE-20538440; PubMed-10948199; Wu H., Xu H., Miraglia L.J., Crooke S.T.; "Human RNase III is a 160-kDa protein involved in preribosomal RNA processing."; J. Biol. Chem. 275:36957-36965(2000). [2] SEQUENCE OF 166-613 FROM N.A. (ISOFORM 2). TISSUE-Colon; MEDLINE-20431278; PubMed-10976766; Gunther M., Laithier M., Brison O.; "A set of proteins interacting with transcription factor Spl identified in a two-hybrid screening."; Mol. Cell. Biochem. 210:131-142(2000).	HUMAN RNC_HUMAN STANDARD; PRT; 1374 AA. Q9NR74; Q9NW73; Q9Y2V9; Q9Y4Y0; Q1-MAR-2002 (Rel. 41, Created) O1-MAR-2002 (Rel. 41, Last sequence update) O1-MAR-2002 (Rel. 41, Last annotation update) Ribonuclease III (EC 3.1.26.3) (RNase III) (p241). RNASE3L OR RN3. HOMO Sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID=9606;

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EMBL; AJ242976; CAB45133.1; -.

EMBL; AJ242976; CAB45133.1; ALT_INIT.

EMBL; AF001121; BAA91511.1; ALT_FRAME.

InterPro; IPR001159; DS_RBD.

InterPro; IPR000359; RNase_3.

Pfam; PF00035; Gsrm; 1.

Pfam; PF00035; RIBOnuclease_3; 2.

SMART; SM00358; DSRM; 1.

SMART; SM00358; DSRM; 1.

SMART; SM00535; RIBOc; 2.

PROSITE; PS50137; DS_RBD; 1.

PROSITE; PS50137; RNASE_3_1; 2.

PROSITE; PS50142; RNASE_3_2; 2.

RIBOSOME blogenesis; Hydrolase; Nuclease; En RNA-binding; Nuclear protein; Alternative sp DOMAIN

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                     KRARWEEEKDRWSDNQSSGKDKNYTSIKEKEPEETMPDKNEEEEEELLKPVWIRCTHSEN
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ARG-RICH.

RNASE III 1.

RNASE III 1.

RNASE III 2.

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ISOFORM 2).

YOYPPGYSH -> RERERTSLE (IN REF. 2).

L -> P (IN REF. 2).

R -> P (IN REF. 1).

R -> T (IN REF. 1).

R -> T (IN REF. 1).

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SHHLNFGMNPDHARNSLSNCGIRQPKYGDRKVHHMHMRKKGINTLINIMSRLGQDDPTPS
                                                                                                            KARRTGIRHSIYPGEEAIKPCRPMTNNAGRLFHYRITVSPPTNFLTDRPTVIEYDDHEYI
                                                                                                                                                                                             YYSSDPMDQVGDSTVVGTSRLRDLYDKFEEELGSRQEKAKAARPPWEPPKTKLDEDLESS
                           KARRTGIRHSIYPGEEAIKPCRPMTNNAGRLFHYRITVSPPTNFLTDRPTVIEYDDHEYI
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               1320
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RESULT 2

RNC_CAEEL STANDARD; PRT; 10

RNC_CAEEL STANDARD; PRT; 10

AC 001326; 001327; Q9U9Q8;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-MAR-2002 (Rel. 41, Last sequence up 01 MAR-2002 (Rel. 41, Last annotation DE Ribonuclease III (EC 3.1.26.3) (RNase

update) ion update) ase III).

1086 AA

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Best Local S
Matches 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See it or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lightning
Submitted
                                                                                                                                                                                                                                                                                              PROSITE; PS50137; DS_RBD; 1.
PROSITE; PS00517; RNASE_3_1; 2.
PROSITE; PS50142; RNASE_3_2; 2.
Ribosome biogenesis; Hydrolase; Nuclease; RNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- FUNCTION: Involved in pre-rRNA processing. Cleaves double RNA and does not cleave single-strand RNA (By similarity)
-i- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 227-1086 FROM N.A.
MEDLINE-20179701; PubMed-10713462;
Filippov V., Solovyev V., Filippova M., Gil
"A novel type of RNase III family proteins
Gene 245:213-221(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lightning
Submitted
                                                                                                                                                                                                                                                                                   RNA-binding;
                                                                                                                                                                                                                                                                                                                                                              SMART; SM00358; DSRM; 1.
SMART; SM00535; RIBOC; 2
                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00035; dsrm; 1.
Pfam; PF00636; Ribonuclease_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F26E4.10 OR F26E4.13.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001159; DS_RBD.
InterPro; IPR000999; RNase_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
                                                                                                                                                                                  Local 364;
             419
                                     111
                                                               389
                                                                                       74
                                                                                                                                           14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphomonoester.
SUBCELLULAR LOCATION: Nuclear (Probable).
SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING)
SIMILARITY: CONTAINS 2 RNASE III DOMAINS.
                                                                                                                                        KHKRARRKKYQKEYQERHKEEMMQQLGRRFQNQPSTSSAPPDTVEKIPLPTESTSALPFG
                                                                                                                                                                RHRSYERSRERERHRHRDNRRSPSLERSYKKEYKRSGRSYGLSVVPEPAGCTPELP-G
             ;
                                    AEEAEKYMMIKAKSTTSKILQDFQTKILETVKTKRRLQADVPYIIHPCHSMKGRKTPKQK
                                                    EKEPEETMPDKNEEEEEELLK-----
                                                                                       DSPRLTEKDYETNYMIDPP--VVSTHSAELIK---
                                                                                                              EIIKNTDS-----WAPPLEIVNHRSPSREKKRARWEEEKDRWSDNQSSGKDKNYTSIK
ENYYSSDPMDQVGDSTVVGTSRLRDLYDKFEEELGSRQEKAKAARPP--WEPPKTKL
                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      j J.;
1 (OCT-1996)
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(OCT-2001)
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                                                                                                                                                                                           206;
                                                                                                                                                                                          Score 1448; DB 1;
Pred. No. 5.7e-65;
6; Mismatches 431;
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                                                                                                                                                                                                                                                                    RNASE III 1.
RNASE III 2.
                                                                                                                                                                                                                                                            DRBM
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                                                                                                                                                                                                                                                                                                             Endonuclease;
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RESULT 3
RNC_BACSU
ID RNC_B
AC P5183
DT 01-OC
DT 30-MA

STANDARD;

PRT;

249 AA

RNC_BACSU S P51833; O31734; O1-OCT-1996 (Rel 30-MAY-2000 (Rel

(Rel. 34, Rel. 39,

Created) Last sequ

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                                                                                                                                                                          KTLQTVGPSHARTYTVAVYFKGERIGCGKGPSIQQAEMGAAMDALEKYNFPQMAHQKRFI 1344
                                                                                                                                                                                                                                                                                                          AALYTDKDLEYVHTFMNVCFFPRLKEFILNQDWNDPKSQLQQCCLTLR-TEGKEPDIPLY
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                                                        GRKYRQELKEMRWEREHQEREPDETED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HHFEGGLATYRTALVQNRNLATLAKNCRIDEMLQYSHGADLINVAEFKHALANAFEAVMA 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLEEGGLATYRTAIVQNQHLAMLAKKLELDPFMLYAHGPDLCRESDLRHAMANCFEALIG 1049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRADWFERDEEKKEV----YVVHNAIRAQTYTAISLPRIAFLEKTLNKMIQ-EKQSSGVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVQLWSSKTVLAYFTSKGSSEIMSPEDVNRLCDAQIDQFTRNTSKHKQSIVLNTKFKPSA 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKEVLSMHQILLYLL-RCSKALVPEEEIANMLQWEELEWQKYAEECKGMIVTNPGTKPSS 751
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-MKAKNNSWFQNMRRRLEQDTSD
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Matches 85
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InterPro; IPR000999; RNase_3.
Pfam; PF00035; dsrm; 1.
Pfam; PF00636; Ribonuclease_3; 1
SMART; SM00358; DSRM; 1.
SMART; SM00358; RIBOC; 1.
                                                                                                                                                                                                                              1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DBB databases.
-!- FUNCTION: DIGESTS DOUBLE-STRANDED RNA. INVOLVED IN THE PROCESSING
OF RIBOSOMAL RNA PRECURSORS AND OF SOME MENAS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene
[2]
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"The effect of Srb, a homologue of
subunit, on Bacillus subtilis grow
Gene 172:17-24(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D64116; BAA10976.1; -. EMBL; Z99112; CAB13466.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus/Staphylococcus
NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SubtiList; BG11537; rnc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96257247;
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  137
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SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphomonoester.
                                                                                                                  LFIHFPDHHEGHLTLLRSSLVNNRTQAKVAEELGMQEYAITNDKTKRPVG-LRTKTLADL 1220
                                                                                                                                                                                                                            LQKLTEFEEAIGVIFTHVRLLARAFTLRTVGFNHLTLGH--NQRMEFLGDSIMQLVATEY 1161
                                                                                                                                                                                 VEQFKEFQERISVHFQNEKLLYQAFTHSSYVNEHRKKPYEDNERLEFLGDAVLELTISRF
FEAFIGALYLDQGLEPVESFLKVYVFPKINDGAFSHVM-DFKSQLQE---YVQRDGKGSL
                                        LESFIAALYTDKDLEYVHTFMNVCFFPRLKEFILNQDWNDPKSQLQQCCLTLRTEGK---
                                                                                        LFAKYPAMSEGDLTKLRAAIVCEPSLVSLAHELSFGDLVLLGKGEEMTGGRKRPALLADV
                                                                                                                                                                                                                                                                              85;
                                                                                                                                                                                                                                                                                            Similarity
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PS00517; RNASE_3_1;
PS50142; RNASE_3_2;
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                                                                                                                                                                                                                                                                                                                                                                                          ## FIND PRINCIPAL SEPTION | FIND PRINCIPAL SEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            group; Bacillus
                                                                                                                                                                                                                                                                           46;
                                                                                                                                                                                                                                                                                                                                                                                       DRBM.
A ->
S ->
Q ->
                                                                                                                                                                                                                                                                                                 Score 315; DB 1; Pred. No. 2.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atsu H., Nakamura K., Yamane K.;
ue of the mammalian SRP receptor a
growth and protein translocation.
                                                                                                                                                                                                                                                                                                                                                                    -> P (IN REF. 1).
-> P (IN REF. 1).
-> E (IN REF. 1).
-> QLNPPYDSGGFQYVCRLI (IN REF.
304F3BOBF5B7CCDC CRC64;
                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA-binding;
III.
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                                                                                                                                                                                                                                                                           96;
                                                                                                                                                                                                                                                                                                                    Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete
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                      Query Match
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  Matches
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STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Alchardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULMAN LOCALINE 1 DRBM (LOCALINE -!- SIMILARITY: CONTAINS 1 RNASE III DOMAIN.
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                                                                                                                                                                                                                                                                       SMART;
SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as lon modified and this statement is not remove entities requires a license agreement (Sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 406:477-483(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNC OR VC2461
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16-OCT-2001
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                                                                                                                                                                                              PROSITE; PS50137; DS_RBD; 1.
PROSITE; PS00517; RNASE_3_1; 1.
PROSITE; PS50142; RNASE_3_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- FUNCTION: DIGESTS DOUBLE-STRANDED RNA. INVOLVED IN THE OF RIBOSOMAL RNA PRECURSORS AND OF SOME MRNAS (BY SIMII -i- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
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16-OCT-2001
                                                                                                                                                                       Hydrolase;
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                                                                                                  SEQUENCE
                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                          Pfam;
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InterPro; IPR000999;
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SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SUBCELLULAR LOCATION: LORBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPDIPLYKTIQTYGPSHARTYTYAVYFKGERIGCGKGPSIQQAEMGAAMDALEKYNFPQM 1337
                                                                                                                                                                                                                                                                                                                       PF00035; dsrm; 1.
PF00636; Ribonuclease_3;
                                                                                                                                                                                                                                                                                                                                                                                                                          VC2461
                                                                                                                                                                                                                                                                                                                                                                                                                                              AE004316; AAF95603.1;
                                                                                                                                                                                                                                                                       SM00358; DSRM; 1.
SM00535; RIBOC; 1
  Similarity
75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1342
                                                                                                Nuclease; Endonuclease;
5 127 RNASE
154 224 DRBM.
225 AA; 25010 MW; 692E
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3.8%;
nilarity 32.2%;
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(Rel. 40, Last annotation update)
E III (EC 3.1.26.3) (RNase III).
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                                                                                                                                                                                                                                                                                                                                                                                                   DS_RBD
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     42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is not removed.
Score 285.5; DE Pred. No. 6e-08; 2; Mismatches 1
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                                                                                                     692FEE74C580990C CRC64;
                                                                                                                                                RNA-binding; Complete III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Long
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May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., K
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-1- FUNCTION: DIGESTS DOUBLE-STRANDED RNA. INVOLVED IN THE
                                                                                                                                                                                SMART; SM00358; DSRM; 1.

SMART; SM00355; RIBOC; 1.

PROSITE; PS50137; DS_RBD; 1.

PROSITE; PS00517; RNASE_3_1; 1.

PROSITE; PS50142; RNASE_3_2; 1.
                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
              1105 QKLTEFEEAIGVIFTHVRLLARAFTLRTVGFNHLTLGHNQRMEFLGDSIMQLVATEYLFI 1164
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat Ribonuclease III (EC 3.1.26.3) (RNase III).
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                                                                                                                         SEQUENCE
                                                                                                                                        DOMAIN
                                                                                                                                                      Hydrolase; Nuclease; Endonuclease; RNA-binding; Complete proteome DOMAIN 5 127 RNASE III.
                                                                                                                                                                                                                                                           Pfam; PF00035; dsrm; 1.
Pfam; PF00636; Ribonuclease_3;
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InterPro; IPR000999;
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Pasteurella.
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SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN.
SIMILARITY: CONTAINS 1 RNASE III DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF RIBOSOMAL RNA PRECURSORS AND OF SOME MRNAS (BY CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphomonoester.
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                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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 QNLERLQRQIGYQFNQPALLKQALTHRSA----
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                                                                           Similarity
                                                                                                                        225 AA;
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                        25461 MW;
                                                                         3.8%;
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                                                           44;
                                                                        Score
Pred.
                                                                                                                                     DRBM
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                                                            Mismatches
                                                                                                                      202B6ACCA562B31C CRC64;
                                                                         282; DB 1;
No. 8.9e-08;
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-AVKHNERLEFLGDAILNFIIAEALYH
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                                                         Gaps
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RESULT 6
RNC_BACHD
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Query Match
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Matches 77
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacteria; Firmicutes; Bacillus group; Bacillus.
                                                                                                               SMART; SM00358; DSRM; 1.
SMART; SM00355; RIBOC; 1.
PROSITE; PS50137; DS_RBD; 1.
PROSITE; PS00517; RNASE_3_1;
PROSITE; PS50142; RNASE_3_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of the alkaliphilic bacterium Bac halodurans and genomic sequence comparison with Bacillus su Nucleic Acids Res. 28:4317-4331(2000).

-I- FUNCTION: Digests double-stranded RNA. Involved in the of ribosomal RNA precursors and of some mRNAS (By simil
                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM 9153;
STRAIN=C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
Medami H., Nakasone K., Takaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Ribonuclease III (EC 3.1.26.3) (RNase III).
                                                                                                                                                                                                                                     EMBL; AP001515; BAB06208.1; -.
InterPro; IPR001159; DS_RBD.
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                                                           SEQUENCE
                                                                       DOMAIN
                                                                                        DOMAIN
                                                                                                    Hydrolase;
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Pfam; PF00636; Ribonuclease_3;
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                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN

    -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fuji F., Hirama C.,
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                                                                                                                                                                                                                     InterPro; IPR000999;
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                                                                                                    Nuclease; Endonuclease;
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259
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Nakamura Y., Ogasawara N.,
                                                           30224 MW;
             3.8%;
30.9%;
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Score 282; DB
Pred. No. 1.1e
50; Mismatches
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                              263;
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"Specific expression of a novel cell wall hydroxyproline-rich glycoprotein gene in lateral root initiation.";

Genes Dev. 3:1639-1646(1989).

"I- FUNCTION: HAS A SPECIALIZED STRUCTURAL FUNCTION, POSSIBLY THE MECHANICAL PENETRATION OF THE CORTEX AND EPIDERMIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Extensin precursor (Cell wall hydroxyproline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOBAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1142
                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=CV. XANTHI; TISSUE=Leaf;
MEDLINE=90128263; PubMed=2612909;
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                                                                                                           CHAIN
                                                                                                                                                                   PIR;
                                                                                                                                                                             EMBL; X13885; CAA32090.1;
                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nicotiana tabacum (Common tobacco)
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                 DOMAIN
                                                                                                REPEAT
                                                                                                                          SIGNAL
                                                                                                                                      Hydroxylation.
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                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Extracellular matrix. PTM: EXTENSINS CONTAIN A CHARACTERISTIC REF. SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYU
                                                                                                                                                                                                                                                                                                                  GLYCOSYLATED
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                                                                                                                                                   Cell wall;
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620
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  65406
    ₹.
                                                                  H-A-P-P.
H-A-P-P.
2 X 7 AA
CONTAINS THE SER-PRO(4) REPEATS 3 X APPROXIMATE TANDEM REPEATS.; 641DD2278AB28524 CRC64;
                                                                                                          POTENTIAL.
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RESULT 8
RNC_BUCAI
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Best Local
PROSITE; PS50137; DS_RBD; 1.
PROSITE; PS00517; RNASE_3_1; 1.
PROSITE; PS50142; RNASE_3_2; 1.
Hydrolase; Nuclease; Endonuclease;
                                                                                      InterPro; IPR001159; DS_RBD.
InterPro; IPR000999; RNASe_3.
Pfam; PF00035; dsrm; 1.
Pfam; PF00636; Ribonuclease_3;
                                                                                                                                                                                                      the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by a
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20445173; PubMed=10993077; Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa "Genome sequence of the endocellular bacterial symbiont of Buchnera sp. APS.";
Nature 407:81-86(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium).
                                                           SMART; SM00358; DSRM; 1. SMART; SM00535; RIBOC; 1.
                                                                                                                                                                                                                                                                                          phosphomonoester.
-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-i- SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN.
-i- SIMILARITY: CONTAINS 1 RNASE III DOMAIN.
                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: DIGESTS DOUBLE-STRANDED RNA. INVOLVED IN THE PROCESS OF RIBOSOMAL RNA PRECURSORS AND OF SOME MRNAS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
NCBI_TaxID=118099;
                                                                                                                                    EMBL; AP001118; BAB12968.1; InterPro; IPR001159; DS_RBD
                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
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16-OCT-2001
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16-OCT-2001
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77; Conserv
                                                                                                                                                                                                                                                  the Swiss Institute of Bioinformatics
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
e III (EC 3.1.26.3) (RNase III).
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30.0%;
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Pred. No. 1e
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    RNA-binding; Complete
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Best Local
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Q9CHD0;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 40, Created)
01-MAR-2001 (Rel. 40, Created)
01-MAR-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial contents are not as a statement of the commercial contents are not as a statement of the commercial contents.
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DOMAIN
PROSITE; PS50137; DS_RBD; 1.
PROSITE; PS00517; RNASE_3_1;
PROSITE; PS50142; RNASE_3_2;
                                                       SMART; SM00358; DSRM; 1.
SMART; SM00535; RIBOC; 1
                                                                                                                                         EMBL; AE006313; AAK04900.1; -.
InterPro; IPR001159; DS_RBD.
                                                                                                                                                                                                                                                                                                                      -i- SUBCELLULAR LOCATION: Cytoplasmic (By si-i- SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRA-i- SIMILARITY: CONTAINS 1 RNASE III DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of the lactic lactis ssp. lactis IL1403."; Genome Res. 11:731-753(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21235186; PubMed=11337471;
Bolotin A., Wincker P., Mauger S.,
Weissenbach J., Ehrlich S.D., Soro
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                                                                                        Pfam; PF00636; Ribonuclease_3;
                                                                                                         Pfam; PF00035;
                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                           entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                            -I- FUNCTION: DIGESTS DOUBLE-STRANDED RNA. 1
OF RIBOSOMAL RNA PRECURSORS AND OF SOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVYGEAHNQLFT--IHCKISTISEYLIGTGSSRRKAEQDAAQKALIK 222
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226
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225 I
25737 MW;
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                        FALSE_NEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jaillon O.,
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                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                          cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
.6e-07;
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Coutstation -
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SEQUENCE FROM .... SEQUENCE FROM .... Majabet STRAIN=K12 / MGJ655;

MEDLINE=97426617; PubMed=9278503;

MEDLINE=97426617; PubMett G. III, Bloch C.A., Perna N.T., Buriblattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Riley M., Collado-Vides J., Glasner J.D., Goeden M.A., Rose I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Nuclease; I
DOMAIN 5 13
DOMAIN 160 229
SEQUENCE 231 AA; 20
                                                                                                                                                                                                      Nashimoto
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol.
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01-JAN-1988 (Rel. 06, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Ribonuclease III (EC 3.1.26.3) (RNase
RNC OR B2567 OR Z3848 OR ECS3433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNC_ECOL
                                                                                                                                                                                                                                                                                                                                                     March P.E., Ahnn J., Inou
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=K12 / SB221;
MEDLINE=85269601; P
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                                                                                                                                                                                                                                                   STRAIN-K12;
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-86039802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli 0157:H7.
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                                                                                                                                                                                                                                                                                                                   Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nashimoto H., Uchida
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76; Conserv
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                                                                                                                                                                                                      H., Saito I
(SEP-1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=3903434;
                                                                                                                                                                                                                                                                                                                 13:4677-4685(1985)
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Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science [5]
                                                                                                                                           EMBL;
EMBL;
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SEQUENCE OF 211-226 FROM N.A.
MEDLINE-87067411; PubMed-3097637;
Ahnn J., March P.E., Takiff H.E., Inou
"A GTP-binding protein of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156331; PubMed=11258796;
Mayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Hayashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
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[6]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins."
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Takiff H.E., Chen
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[7]
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0157:H7 and genomic comparison with a laboratory strain K-12.";
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                          InterPro; IPR001159; DS_RBD.
InterPro; IPR000999; RNase_3.
Pfam; PF00035; dsrm; 1.
Pfam; PF00636; Ribonuclease_3; 1.
                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                             between
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                                                                                                                       BL; AE000343; AAC75620.1; -.
BL; AE005487; AAG57682.1; -.
BL; AP002562; BAB36856.1; -.
BL; MZ6415; AAA21843.1; -.
BL; M14658; AAA03241.1; -.
BL; AAA03241.1; -.
                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBURIT: ORGANIZED INTO A STRUCTURE (PROCESSOME) CONTAINING A NUMBER OF RNA-PROCESSING ENZYMES.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN SIMILARITY: CONTAINS 1 RNASE III DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C. Natl. Acad. Sci. U.S.A. 83:8849-8853(1986).
FUNCTION: DIGESTS DOUBLE-STRANDED RNA. INVOLVES
OF RIBOSOMAL RNA PRECURSORS AND OF SOME MRNAS.
CATALYTIC ACTIVITY: Endonucleolytic cleavage to
                                                                                                             A24022;
                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                         X02946; CAA26692.1; -. X02673; CAA26504.1; -. D64044; BAA10914.1; -. U36841; AAA79829.1; -.
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                                                                                            022; NREC3.
EG10857; r
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8:11-22(2001).
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RIBOC; 1.
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STRANDED RNA. INVOLVED IN
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chia coli has homology
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Matches 70
                                                                                                                                         A Sherrington R., Rogaev E.I., Liang Y., Rogaeva E.A., Leves A Ikeda M., Chi H., Lin C., Li G., Holman K., Tsuda T., Mar Foncin J.-F., Bruni A.C., Montesi M.P., Sorbi S., Rainero A Pinessi L., Nee L., Chumakov I., Pollen D., Brookes A., Sanseau P., Pollinsky R.J., Wasco W., da Silva H.A.R., Hain A Pericak-Vance M.A., Tanzi R.E., Roses A.D., Fraser P.E., Rommens J.M., St George-Hyslop P.H.; "Cloning of a gene bearing missense mutations in early-ons: Alcheimer's disease."; Nature 375:754-760(1995).
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PROSITE; PS
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DOMAIN
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MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZAP3_HUMAN STANDARD; PRT; 1822 AA. P49750; P49752; Q9P1V7; 01-OCT-1996 (Rel. 34, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Nuclear protein ZAP3 (ZAP113).
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 539-847
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                                                                                                                     SUBCELLULAR LOCATION: Nuclear ()
CAUTION: Ref.2 sequence differs
                                                                                           frameshift in position 1661
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Fleetwood P., Harrison G., Jan
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III.
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n K., Tsuda T., Mar L.,
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A., Shaffer T.,
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                                                                                                                                                   HSIYP----GEEAIKPCRPMT-----NNAGRLFHYRITVSPPTNFLTDRPTVIEYDD
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                                                                                             HEYIFEGFSMFAHAPLTNIPLCKVIRFNIDYTIHFIEEMMPENFCVKGLELFSLFLFRDI
                                                                                                                                                                                             QSSQVPEKPRPALLPTPVSFGSAPPTTYH-----
                                                                                                                                                                                                                       SDSEVFD-----VIAEIKRKKAHPDRLHDELWYNDPGQMNDGPLCKCSAKA--RRTGIR
                                                                                                                                                                                                                                                       KHTQLQQILQQYQQIIQPPPHIQATTPPPGIPP-----PGVPQGIPPQLTAAPVPPASSS
                                                                                                                                                                                                                                                                                       GTSRLRDLYDKFEEELGSRQEKAKAARPPWEPPKTKLDEDLESSSESECESDEDSTCSSS
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                               LELYDWNLKGPLFEDSPPCCPRFHFMPRFVRFLPDGGKE---VLSMHQILLYLLRCSKAL
                                                                                                                          YSSFSSDQGLGESSAAPSQPITAVKDMPVRSGGLL-----PDPPRSSYLESPRGPRFDG
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L40400; AAC42006.1;
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PRYEGHPAEGTKSKWGMIPRGPASQFYITPSTSL
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8E6CB83FE540C7D2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Glycosylated polyproline II rods-with-kinks plant hydroxyproline-rich glycoproteins.";
Biochemistry 40:2978-2987(2001).
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Eukaryota; Viridiplantae; Chlorop
Chlamydomonadaceae; Chlamydomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01217; PRICHEXTENSN. PRINTS; PR01218; PSTLEXTENSIN.
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InterPro; IPR002965; P_rich_extensn.
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49 X 5 AA APPROXIMATE PPSSX REPEAT:
POLY-PRO.
N-LINKED (GLCNAC. . .) (POTENTIAL)
M-; 6A584A90465502F5 CRC64;
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                                    Score 259.5;
Pred. No. 3.
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SEQUENCE 1386 A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misawa K., Nosaka T., Kitamura T.,
"A huge nuclear protein rich in proline similar to human protein zap3 and zap113.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nuclear protein ZAP3. ZAP3 OR ZAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9R017;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Fetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seg
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZAP3_MOUSE
  104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASR 410
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                                                    LSSATPPPGIPPPGAPQGMPPQLTAPLPPASGSQNSQIPEKPRQALLPTPVSFGSTPPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGI:1926195;
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473
1012
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21.5%;
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Last annotation updat
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GLN-RICH.
ARG-RICH.
                                                                                                                                                                                                                                                                               Score 259.5;
Pred. No. 1e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                              D862F9918ED221DF
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                                                                                                                                                                                                                                                       165;
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                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                        584
     105
                                                       644
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RESULT 14
BRM_DROME
             RX MEDLINE-ZULYBULUN, FLUMING.
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeilfer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Apbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S. M.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Fleischmann W.,
RA Dodson K., Doup L.E., Downes M., Fleischmann W.,
RA Dock M., Ra Dock J., Brocha S., Fleischmann W.,
RA Dock M., Ra Dock J., Broch S., Fleischmann W.,
RA Dock M., Ra Dock J., Broch S., Fleischmann W.,
RA Dock M., Ra Dock J., Broch S., Fleischmann W.,
RA Dock M., Ra Dock J., Broch S., Fleischmann W.,
RA Dock M., Ra Dock J., Broch S., Fleischmann W.,
RA Dock M., Ra Dock J., Broch S., Fleischmann W.,
RA Dock M., Ra Dock J., Broch S., Fleischmann W.,
RA Dock M., Ra Dock J., Broch S., Fleischmann W.,
RA Dock M., Ra Dock J., Broch S., Fleischmann W.,
RA Dock M., Ra
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Homeotic gene regulator (Brahma protein).
BRM OR CG5942 OR CG18438.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1046
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BERKELEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tamkun J.W., Deuring R., Scott M.P., Kaufman T.C., Kennison J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (LONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Brahma: a regulator of Drosophila homeotic related to the yeast transcriptional activat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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K.J., Evangelista C.C.,
C., Gabrielian A.E., Gar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   omeotic genes
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  Gelbart W.M.,
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McShrefi A.,
RA Melson D.R., Melson K.A., Nixon K., Nusskern D.R., Nelson D.L.,
RA Melson D.R., Melson K.A., Nixon K., Nusskern D.R., Nelson D.L.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Sylirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Sylirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., G.M. D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Yelliams S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yelliams S.M., Actor A., Rubin G.M., Venter J.C.,
RT The genome sequence of Drosophila melanogaster.";
RI Science 287:2185-2195(2000)
C. TARNSCRIPTIONEL ACTIVATORS OF ANT-C AND BY-C HOMEOTIC GENES. CAN
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C. SHORT FORM; MAY BE PRODUCTS: 2 ISOFORM; A LONG FORM (SHOWN HERE) AND A
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C. SINILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
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InterPro; IPRO01410, DEAD.
InterPro; IPRO0150; Helicase_C.
InterPro; IPR000330; SNF2_N.
Pfam; PF00439; bromodomain; 1.
Pfam; PF00271; helicase_C; 1.
Pfam; PF00176; SNF2_N; 1.
PRINTS; PR00503; BROMODOMAIN.
PRINTS; PR00503; BROMODOMAIN.
                                                                                                                                                                                                                 PROSITE: PS00633; BROMODOMAIN_1; 1.
PROSITE: PS50014; BROMODOMAIN_2; 1.
Developmental protein; Transcription regulation; Nuclear protein;
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SM00487; DEXDC; 1.
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ASP/GLU-RICH (ACIDIC).
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                                                                                    QASIMVNGTLKEYQIKGLEW-----LVSLYNNNLNGILADEM-
                                                                                                                                                                      VSPPTNFLTDRPTVIEYDDHEYIFEGFSMFAHAPLTNIPLCKVIRFNIDYTIHFIEEMMP
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Biochimie [2]
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                                          MEDLINE=97295239; PubMed=9150881;
Anderson P.E., Matsunaga J., Simons E.L., Simons R.
Structure and regulation of the Salmonella typhimu
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                                                                                                                                                                             Salmonella typhimurium
                                                                                                                                                                                           RNC OR STM2581
                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                 NCBI_TaxID=602;
                                                                                                                                                   Salmonella
                                                                                                                                                              Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---RVLYKHMQSKGV--LLTDGSEKGK------HG----
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                                                                                                                                                                                                                                                                                                                                                        LKAIDDGAEFDEEEEEDDSKRKRRK 1399
                                                                                                                                                                                                                                                                                                                                                                                                                  HPGRERLIDESELPDWLTKDDDEVERFHY--QYDEDTILGRGSRQRKEVDYTDSLTEKEW
                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGKGPSIQQAEMGAAM----DALEKYNFPQMAHQKRFIGRKYRQ-----ELKEMRW 1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILHQDDNEEEEENEVPDDEMINMMIARSEEEIEIFKRMDAERKK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AITNDKTKRPVGLRTKTLADLLESFIAA----LYTDKDLEYVHTFMNVCFFPRLKEF---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTDRQLIETSPYLQKLTEFEEAIG-VIFTHVRL------LARAFTLRTVGFNHLT
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                78:1025-1034(1996)
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                                                                                                                                                                gamma
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                                                                                                                                                                subdivision;
                                             typhimurium
                                                                                                                                                                Enterobacteriaceae;
                                             rnc-era-reco
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                                                                                                                                                               1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: DIGESTS DOUBLE-STRANDED RNA. INVOLVED OF RIBOSOMAL RNA PRECURSORS AND OF SOME MENAS.
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE-21534948; PubMed-11677609;
                                                                                                                                                                                                                                                                      1161 YLFIHFPDHHEGHLTLLRSSLVNNRTQAKVAEELGMQEYAITNDKTKRPVGLRTKT-LAD 1219
                                                                                                                                                                                                                                                                                                                                                                           1101 SPYLQKLTEFEEAIGVIFTHYRLLARAFTLRTYGFNHLTLGHNQRMEFLGDSIMQLVATE 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50137; DS_RBD; 1.
PROSITE; PS00517; RNASE_3_1;
PROSITE; PS50142; RNASE_3_2;
Hydrologo, No. 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00358; DSRM; SMART; SM00535; RIBOC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR001159; DS_RBD.
Interpro; IPR000999; RNase_3.
pfam; PF00035; dsrm; 1.
pfam; PF000636; Ribonuclease_3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of Salmonella LT2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston R., Wilson R.K.;
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SUBUNIT: ORGANIZED INTO A STRUCTURE (PROCESSOME) CONTAINING A NUMBER OF RNA-PROCESSING ENZYMES.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN.
SIMILARITY: CONTAINS 1 RNASE III DOMAIN.
                                            DIPLYKTLQTVGPSHARTYTVAVYFKG--ERIGCGKGPSIQQAEMGAAMDALEK 1331
PLPSYLVVQVRGEAHDQEFTIHCQVSGLSEPV-VGTGSSRKKAEQAAAEQALKK
                                                                                                                                                            LLESFIAALYTDKDLEYVHTFMNVCFFPRLKEFILNQDWNDPKSQLQQCCLTLRTEGKEP 1279
                                                                                                                                                                                                                 ALYHRFPRVDEGDMSRMRATLVRGNTLAELAREFDLGECLRLGPGELKSGGFRRESILAD
                                                                                                                                                                                                                                                                                                                        NPIV--INRLQRKLGYTFNHQELLQQALTHRSASSK-----HNERLEFLGDSILSFVIAN
                                                                                                       TVEALIGGVFLDSNIQTVEQLILNWYKTRLDEISPGDKQKDPKTRLQE-----YLQGRHL
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226 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 258; DB 1;
Pred. No. 1.4e-06;
7; Mismatches 10;
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AT -> DP (IN REF. 1).
EQAL -> NSV (IN REF. 1).
; 5752C0113COA055A CRC64;
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Search completed: October Job time : 41 secs

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Sequence:
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                  4071
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1: /SIDS1/gcgdata/g
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AAR13995	ABG23699	ABG21919	AAU23180	ABB03068	AAB26153	AAR28150	AAG46150	AAG46151	AAG46152	AAW20772	ABB70063	AAM78694	ABG09877	AAE09769	ABB60977	ABB68526	ABG14000	ABG09876	ABB61946	AAG82282	AAW31852	AAW31855	ABG21932	AAY09366	ABB63064	AAM41045	ABB61362	AAM39259	ABB66989	AAW81354	ABG27250	ABG21040	ABB61598
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ALIGNMENTS

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AAB92635 standard; Protein;

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                                                                                  29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                    WPI; 2001-318749/34.
                                                                                                                                                                                                                      Human; primer;
Primer sets for synthesizing polynucleotides, particularly the 5602
                                                                                                                                                               07-FEB-2001.
                                                                                                                                                                                                                                        Human protein sequence SEQ ID NO:10949
                                                                                                                                            28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                 EP1074617-A2.
                                                                                                                                                                                                  Homo sapiens
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                                                                 (HELI-) HELIX RES INST.
                                     Isogai T, Nishikawa T,
, Sugiyama T, Wakamatsı
                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                    detection; diagnosis; antisense therapy; gene therapy.
                                      Wakamatsu
                                     Hayashi K, S
A, Nagai K,
                                      Saito K,
(, Otsuki
                                      Η,
                                               Yamamoto
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The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of CC the 5602 nucleotide sequences defined in the specification, where the CC complementary strand of a polynucleotide which comprises one of CC the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end cC englementary to a combination of CC complementary strand of a polynucleotide which comprises a 5'-end sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC complementary to a complementary to a conjunct of the sequence/3'-end sequence is selected from those defined in CC the 5'-end sequence/3'-end sequence is selected from those defined in CC the 5'-end sequence/3'-end sequence is selected from those defined in CC in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by CC cDNAs easily without any specialised methods. AAH3363 to AAH3362 and CC AAH3583 to AAH38742 represent human cDNA sequences; AAB92446 to CC AAH35893 represent human amino acid sequences; and AAH3629 to AAH3632 cof the present invention.
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MEFIGDSIMQLVATEYLFIHFPDHHEGHLTLLRSSLVNNRTQAKVAEELGMQEYAITNDK
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                                                                                        LQLQEPNTDRQLIETSPVLQKLTEFEEAIGVIFTHVRLLARAFTLRTVGFNHLTLGHNQR
                                                                                                                                          LQLQEPHTDRQLIETSPVLQKLTEFEEAIGVIFTHVRLLARAFTLRTVGFNHLTLGHNQR
                                                                                                                                                                                                     HGPDLCRESDLRHAMANCFEALIGAVYLEGSLEEAKQLFGRLLFNDPDLREVWLNYPLHP
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                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventi useful in developmental biology and in elucidating cell signalling a cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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inappropriate expression of secreted proteins. (I) and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and so which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of the secreted proteins. The anti-(II) antibodies and antagonists may also be used to down regulate expression and activity of (II). The anti-(II) antibodies may also be used as diagnostic agents for detecting the presence of (II) in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The
                                                                                                                                                                                encoding human secreted proteins (II). (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used it the prevention, treatment and diagnosis of diseases associated with
                                                                                                                                                                                                                                                                                  Claim
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Gaucher's disease; neurological
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rheumatoid arthritis; antiarteriosclerotic;
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cerebrovascular disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders include for example: immune/autoimmune diseases (e.g. HIV human immunodeficiency virus) infections, anaemia, rheumatoid arthrand multiple sclerosis), cancers and hyperproliferative disorders (e melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease and Charcot-Marie-Tooth disease), cardio-/
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                                                                                                                                                                                                                                     hyperproliferative muscular disorder;
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                                                            WO200155163-A1
                                                                                                                                                                                                   Human; neoplastic disease associated polypeptide; cancer; hyperpoliferative disorder; neural disorder; immune system neural disorder; gastrointestinal d pulmonary disorder; cardiovascular disorder; renal disorder;
                                                                                                                                                                                                                                                                                                                                                 Novel human neoplastic disease associated polypeptide #177
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                                                                       Rosen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of disorders involving neoplastic disease such as hyperproliferative disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem glioma, adult liver cancer, childhood cerebellar astrocytoma, or Hodykin's lymphoma). The sequences of the invention may also be useful for treating other disorders such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders and renal disorders. The polynucleotide sequences of the invention are also useful in gene therapy. AAO/21568-AAO/21851 represent the novel human neoplastic disease associated polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                    AAU20385;
                                                                                                                                                      AAU20385 standard; Protein; 378
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                                                                                                                                                                                                                                           WEREHQEREPDETEDIKK 378
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nilarity 98.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ion relates to the isolation of novel human neoplastic polypeptides, and cDNA (AAS34767-AAS35050) and DNA for these polypeptides. The sequences of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       687pp; English
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Pred. No. 5.3e-131;
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Immunomodulatory; human immunodeficiency virus; HIV; anaemia; rheumatoid arthritis; antiarteriosclerotic; cardiant; vascula;

angina;

Human 06-DEC-2001

secreted

protein, Seq ID No

377.

(first entry)

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CC encoding human secreted proteins (II). (I) and (II) are used to prevent, CC treat or ameliorate a medical condition in e.g. humans, mice, rabbits, CC goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in CC inappropriate expression of secreted proteins. (I) and complementary CC sequences may also be used as DNA probes in diagnostic assays (e.g. CC polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and so which patients may be in need of restorative therapy. (II) may also be used as antigens in CC dayonists and antagonists of the expression and activity of the secreted proteins. The anti-(II) antibodies and antagonists may also be used to CC down regulate expression and activity of (II). The anti-(II) antibodies and antagonists may also be used to CC may also be used as diagnostic agents for detecting the presence of (II) samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis cand multiple sclerosis. Cancers and humansorbiforative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              cerebrovascular disorders (e.g. cardiac arrest, tachycardia, angina and thrombosis), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). (I) and (II), agonists, antagonists and antibodies can also be used to promote wound healing, maintain organs before transplantation, and support cell culture of primary tissues. ANU2031-ANU2066 represent human secreted protein amino acid sequences, and related sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary Syndrome and Gaucher's disease, neurological diseases (e.g. Alzheimer's disease, Parkinson's disease and Charcot-Marie-Tooth disease), cardio-/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                  ATYRTAIVQNQHLAMLAKKLELDPEMLYAHGPDLCRESDLRHAMANCFEALIGAVYLEGS 1056
   LEEAKQLFGRLLFNDPDLREVWLNYPLHPLQLQEPNTDRQLIETSPVLQKLTEFEEAIGV
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98.7%;
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Pred. No. 1.2e-130;
0; Mismatches 5;
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                                                                                                                                                                                                                                                                                        Length
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26-JUL-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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07-JUL-2000;
07-JUL-2000;
                                                                                                                                                                                                                                    04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                     hyperproliferative disorder; neural disorder; immune system disorder muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; rehal disorder;
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28-JUN-2000;
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                                                                                             14-JUL-2000;
26-JUL-2000;
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19-MAY-2000;
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17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                            neuroprotective;
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                    2000US-0198123

2000US-0205515

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2000US-0214886

2000US-0216647

2000US-0216647

2000US-0211680

2000US-0217487

2000US-0218290

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2000US-0186350.
2000US-0189874.
2000US-0190076.
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                                                                                                                                                                                                                                                                                          2001WO-US01358
                                                                                                                                                                                                                                                                                                                                                                           cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                             anti inflammatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide;
                                                                                                                                                                                                                                                                                                                                                                                                                      cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                           disorder;
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14-SEP-2000
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14-SEP-2000
14-SEP-2000
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29-SEP-2000

29-SEP-2000

29-SEP-2000

02-CCT-2000

03-CCT-2000

04-CCT-2000

05-CCT-2000

06-NOV-2000

08-NOV-2000

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22 AUG 2000

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23 AUG 2000

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01 - SEP 2000
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2000US-0225759
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08 NOV 2000
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N-PSDB;
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DB; AAS34779.
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Novel polypeptides and polynucleotides useful as diagnostic reagents diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, and for treating cancers, rheumatoid arthritis ç

Claim 11; SEQ IJ ŏ 307; 687pp; English.

The present invention relates to the isolation of novel human neoplastic disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of disorders involving neoplastic disease such as hyperproliferative disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem glioma, adult liver cancer, childhood cerebellar astrocytoma, or Hodgkin's lymphoma). The sequences of the invention may also be useful for treating other disorders such as neural disorders, immune system disorders, pulmonary disorders, cardiovascular disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders and renal disorders. The polynucleotide sequences of the invention are also useful in gene therapy. ANU21568-ANU21851 represent the novel human neoplastic disease associated polypeptides of the invention.

Note: The sequence data for this patent did not form part of the printed as friction, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences

Sequence

17.6%; Score 1320; DB 22; Length 263;

22;

Length

301;

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 Sequence
                                    represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucle acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein
                                                                                                 AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively. AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
                                                                                                                                                                                                                                                             WPI;
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10-SEP-1999;
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99US-0153454
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0; Mismatches 6;
                                                                                                                                                                                                       , gastric and prostate cancer associated diagnosing and treating a condition an abnormal amount of a protein, e.g.
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Best Local Similarity
                     represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nuacids or anti-CAAP antibodles are useful for diagnosing and treating condition characterised by expression of an abnormal amount of a protein condition characterised by expression of an abnormal amount of a protein respectively.
                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding breast, antigen precursors, useful for characterized by expression of a
                                                                                                                                                      represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively. AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
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10-SEP-1999;
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                                                                                                                                                                                                                                                                                         Example 1;
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                  represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively. AAB63232 to AAB63468 to AAB63721 and AAB63722 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nu
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Best Local S
Matches 231
                                                                                                                                                                                                                                                                                                                    Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
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                                                            New nucleic acids encoding human secreted proteins -cDNA libraries prepared from kidney, fetal kidney, demuscle, muscle and heart tissue
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                                       Claim 34;
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                                                                                                            1999-153784/13
DB; AAX41057.
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Pred. No. 1.4e-71;
5; Mismatches 21;
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AAY01602 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 3' different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained
                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedure
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                                                                                                                                                                            Claim 13; SEQ ID 4635; 71pp + CD-ROM;
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.2e-27;
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                                                                                                                                                                                                                                  mapping procedures
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                                                                                    a large number
s. The 5' ESTs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from oligo-dT 'primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                     genes from Drosophila
                                                                                                                                                                                                  New isolated nucleic
                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                      Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                     23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                     WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 11586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB61598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB61598 standard; Protein; 1151 AA
                                                                                                                                                                           interactions
                                                                                                                                                                                                                                                                             (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      511 KKAHPDRLHDELWYNDPGQMNDGPLCKCSAKARRTGIRHSIYPGEEAIKPCRPMTNNAGR 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 LFHYRITVSPPTNFLTDRPTVIEYDDHEXIFE 115
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                                                                                                                                                                                                                                   2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRXNLDRLHDELWYNDPGQMNDGPLCKCSAKARRTGIRHSIYPGEEAIKPCRPMTNNAGR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88;
                                                                                                                                                                                                                         ABL05701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                    2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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95.7%;
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                                                                                                                                                                                                                                                        PWD,
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for elucid
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Pred. No. 1.
                                                                                                                                                                                     ection reagent for detecting elucidating cell signalling
                                                                                                                                                                                                                                                       Myers
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.2e-27;
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                                                                                                                                                                                     cell-cell
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insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from

format directly

from

WIPO

(ABB57737-ABB72072).

at ftp.wipo.int/pub/published_pct_sequences

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of

invention

S

and

Disclosure; SEQ

ID NO 11586;

21pp + Sequence Listing; English

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ABG21040
ID ABG211
XX ABG21
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                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
      Homo sapiens
                                                                                                     Novel human diagnostic protein #21031.
                                                                                                                                               18-FEB-2002
                                                                                                                                                                                       ABG21040;
                                                                                                                                                                                                                           ABG21040 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                628 TIHFIEEMMPENFCVKGLELFSLFLFRDILELYDW-----NLKGPLFED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 --PGQGTFPFMMPPPSMPHPP----PPPVMPQQVNYQYPP-----GY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 RPASPKVEPP-----PPAPPGVESPPGPQPPASPRFDPPPPHTIEPPPPPAPPTLVPPP 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 RPSAPSFRPQNLRLLHPQQPPVQYQYEPPSAPSTTFSNSPAPNFL-----PPRPDFVPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                            VTHF-EENTDE------FRTRLQLINQLIEDRKNLLNRLSED 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKES-MDTLEDE------KVETNVEEN--KSEEESKP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QPEDSAATMKSDAPVENANGTNGNSNGSTNGACDNVSGVVIVSDILQQSTSSFVELTAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDHDRGRDRDRNKSNTSGSAENKAIHDDHSESKEKYKQRRGSDSNDEGKPPSSGGPAKNS
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                                                                                                                                                                                                                                                                                                                                                                                                          -----PQDADKPATPVPISNEQSDEFSADF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEKAKAARPPWEPPKTKLDEDLESSSESECESDEDSTCSSSSD-----SEVFDVIAEIK 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEEEE----LLKPVWIRCTHSENYYSSDPMDQVGDS----TVVGTSRLRDLYDKFEEELGSR 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----EYKRSGRSYGLSVVPEPAGCTPELPGEIIKNTDSWAPPLEIVNHRSPSREKKRAR 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSSSSKHSSSNSSSSKHKSSSSKNDKSSSSSSSRSNRESSSSKRSGTTSSSRHESSSHKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRYRSDYDRGR-TPSRHRSYERSRERERERHRHRDNRRSPSLER-----SYKK 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----KSHSKSRDKEKEKDRRHHRHSDDKH----RRRSTDRDRDRSRDKSHSKHS
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173; Conserv
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Pred. No. 3.1e-15;
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W W0200175067-A2.

XX 11-OCT-2001.

XX 11-OCT-2001.

XX 30-MAR-2000; 2000US-0540217.

XX 31-MAR-2000; 2000US-0649167.

XX 23-AUG-2000; 2000US-0649167.

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The invention relates to isolated polynucleotide (I) and CD polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostices as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (CI). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical company of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capponsible for genetic disorders or other traits to assess biodiversity and oacid sequences. ABG00010-ABG30377 represent novel human call as equence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO cat fip. wipo.int/pub/published_pct_sequences.

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                       APNELPPRPDFVPFP-----PSAQ----PSAQ---GPLPPCPIRPPFPNHQMR 108
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                                                      RNRATSSSAISRAVSDASAGVDYGSAIETLVTAISLIKTIPKYP----ADDRCTKFLISS
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                                                                                                                                                                PPTNSGMPTSDSRGPPPTDP----YGRPPPYDRGDYGPPGREMDTARTPLSEAEFEEIMN
                                                                                                                                                                                                                       PPSMPHPP-----PPPVMPQQVNYQYPPGYSHHNFPPP-----SFNSFQN 187
                                                                                                                                                                                                                                                                          PPGPPPPQQGPPPPPGPPPRPTGSNLGHPLTLAPPSASFPGPPPGAPPPSPHVNPAFFP 368
-HRHRDHSHGRGERHRSLDRRERGRSPDRRRQDSRYRSDYDRGRTPSRHRSYERSR
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                                                                                                             -----FRHLPPYPLPKAPSERRSPERLKH
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                                                                                                                                   polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human
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Matches
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                                                            Sequence
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23-AUG-2000; 2000US-0649167
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                                                                                                            specification,
                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
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B; AAS91437.
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upplement; medical imaging; diagnostic; genetic disorder.
87; Conser
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Score 303.5;
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AAW81354 standard;
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                                                                                                                                                                                                                                                                                                                                          Ribonuclease III; rnc; antibacterial agent; S. pneumoniae infection; meningitis; adhesion inhibitor; extracellular matrix protein;
                                                                                                                                                                                                                                                                                                                                                                                       19-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                       AAW81354;
                                                                                                              Claim 12; Page 6; 22pp; English.
                                                                                                                                               New isolated nucleic acid encoding rnc protein of Streptococcus pneumoniae - and related vectors, transformants, antibodies,
                                                                                                                                                                         N-PSDB; AAV68458
                                                                                                                                                                                  WPI; 1999-011652/02.
                                                                                                                                                                                                                                               05-JUN-1997;
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                                                                                                                                                                                                                                                                                                                  Streptococcus
                                                                                                                                       proteins, and antagonists,
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                                                                                                                                                                                                                                                                                                                                    infection diagnosis.
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This sequence is the Streptococcus pneumoniae ribonuclease III (rnc) protein of the invention. Cells containing the DNA are used to express rnc which is useful therapeutically; to screen for compounds that interact with, and activate or inhibit, it (potential antibacterial agents) and to generate antibodies (Ab) (including as vaccines to provide a protective response). The protein and its agonists are used to treat conditions where rnc polypeptide is required and the antagonists where rnc polypeptide is required and the antagonists where rnc polypeptide of inhibited, particularly a wide range of infections caused by S. pneumoniae, most particularly meningitis. The rnc protein also inhibit adhesion of bacteria to extracellular matrix

proteins, in-dwelling devices and wound with expression of rnc are diagnosed: (

nd surfaces. Diseases (a) by analysing a sa

associated for

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                                                                                                                                                                                                                                                                        presence of the protein; or (b) by detecting nucleic acid encoding the protein. Ab are useful as antibacterial agents; to isolate or identify rnc-expressing clones and for affinity purification. Fragments of the DNA are useful as probes or primers to isolate full-length or related sequences; to screen for drugs, and to diagnose or stage infections, also for genotyping and serotyping of infective agents (e.g. by detecting
                            1224 FIAALYTOKOLEYVHTEMNVCFFPRLK--EFILNQDWNDPKSQLQQCCLTLRTEGKEPDI 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
176 AIRYQVISETGPAHDKVFDVEVLVEGKSIGQGQGRSKKLAEQEAAKNAVEK 226
                                                                                        125 FLGALLLDKDVAKVKEFIYQVMIPKVEAGEFEMITDY---KTHLQE---LLQVNG---DV 175
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US-08-574-959A-7
US-09-357-014-7
US-09-357-014-7
US-09-323-735-4
US-08-818-111-1138
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4 US-08-478-029A-65 2 US-08-290-731C-2 2 US-08-290-731C-2 2 US-08-290-731C-6 1 US-08-27-536-2 1 US-08-27-536-2 5 PCT-US95-04682-2 4 US-09-356-952-2 1 US-09-356-952-2 1 US-09-356-952-2 2 US-07-638-431-2 5 PCT-US92-00018-2 5 PCT-US92-00018-2 6 PCT-US92-00018-2 6 PCT-US92-00018-2 7 US-09-150-4608-6 5 PCT-US92-00218-2 6 US-09-150-4608-10 6 US-09-150-641-5 7 US-09-200-641-5 7 US-09-303-664-54
US-08-290-731C-2 US-08-290-731C-2 US-08-290-731C-6 US-08-290-731C-6 US-08-297-736-2 PCT-US95-04682-2 US-09-041-886-19 US-09-356-952-2 US-09-356-952-2 US-09-356-952-2 US-09-150-4608-6 PCT-US92-00018-2 US-09-150-4608-10 US-09-200-481-5 US-09-200-731C-4 US-09-303-064-54

ALIGNMENTS

RESULT 1 US-08-869-674-2 US-08-869-674-2 Sequence 2, Application US/08869674 Patent No. 5866365 Matches Query Match Best Local : INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 232 amino acids GENERAL INFORMATION: NAME: Bloom, Allen REGISTRATION NUMBER: 29,135 REFERENCE/DOCKET NUMBER: GM10 TELECOMMUNICATION INFORMATION: TELEPHONE: 609-520-3214 TELEFAX: 609-520-3259 ZIP: 08543 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FASTSED for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/869,674 FILING DATE: NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: ADDRESSEE: Dechert Price & Rhoads STREET: 997 Lenox Drive, Building 3, CITY: Lawrenceville APPLICANT: Lonetto, Michael A. APPLICANT: Rosenberg, Martin TITLE OF INVENTION: NOVEL COMPOUNDS FILING DATE: ATTORNEY/AGENT INFORMATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: STREET: CITY: La STATE: 1 COUNTRY: TYPE: amino acid STRANDEDNESS: sir TOPOLOGY: linear Local Similarity hes 75; Conserv TELEX: CLASSIFICATION: 436 Ϋ́ USA Conservative single 3.7%; Score 277.5; DB 2; 32.5%; Pred. No. 3.6e-14; 7. Mismatches 92; 2 GM10013 Suite Length Indels 17; 232;

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1108 TEFEEAIGVIFTHVRLLARAFTLRTVGFNH--LTLGHNQRMEFLGDSIMQLVATEVLFIH 1165

FLGALLLDKDVAKVKEFIYQVMIPKVEAGEFEMITDY---KTHLQE----LLQVNG---DV

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SEQUENCE CHARACTERISTICS:
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1166 FPDHHEGHLTLLRSSLVNNRTQAKVAEELGMQEYAITNDKTKRPVGLRTK--TLADLLES 1223
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
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nes 75; Conserv
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REGISTRATION NUMBER: 29,135
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                                                YPKKPEGDLSKLRAMIVREESLAGFARDCQFDQF-IKLGKGEEKSGGRNRDTILGDAFEA 124
                                                                                                              TVLKNHFAIEFADKNLLETAFTHTSYANEHRLLKISHNERLEFLGDAVLQLLISEYLYKK
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997 Lenox Drive, Building 3, Suite 210
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ROSENDERG, MATTL...
ROYEL COMPOUNDS
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linear
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Patent No.
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Best Local :
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NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,
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APPLICANT: Warren, Richard L
TITLE OF INVENTION: NOVEL RD
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1266 QQCCLTLRTEGKEPDIPLYKTLQTVGPSHARTYTVAVYEKGERIGCGKGPSIQQAEMGAA 1325
                                                                                                                                                                                                                                             1092 NTDRQLIETSPVLQKLTEFEEAIGVIFTHVRLLARAFTLRTV--GFNHLTLGHNQRMEFL 1149
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                                                                                          1210 VGLRTK--TLADLLESFIAALYTDKDLEYVHTFMNVCFFPRLKEFILNQDWN--DPKSQL 1265
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TOPOLOGY: li
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OPERATING SYSTEM:
SOFTWARE: FastSEC
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                                                        TGGRTRPSLISDAFEAFIGALYLDQGLDIVWKFAEKVIFPHVEQ----NELLGVVDFKTQF 177
                                                                                                                               GDAVLELTYSRYLFDKHPNLPEGNLTKMRATIVCEPSLVIFANKIGLNEMILLG-KGEEK 120
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4000 Bell Atlantic Tower,
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Marra, Andrea
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Pred. No. 2.6e-13;
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                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, IN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1326 MDALEK 1331
                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                            STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 PLPKAPSERRSP 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 PPSAPSTTESNSPAPNELPPRPDEVPEPPPMPPSAQGPLPPCPIRPPEPNHQMRHPPPVP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54
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                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 13-SEP-1984
SOFTWARE:
                          COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --QYPPGY-SHHNFPP-----PSFNSFQNNPSSFLPSANNSSS------PHFRHLPPY 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCFPPMPPPMPCPNNPPVPGAPPGQGTFP--FMMPPPSMPHPPPPPVMPQQVNY----- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPAPPAPAFAPAALAPAPPNPN--PQSPPSPPTP-PPTPPSPPAP------PSP 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P----PTYKAKP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPSPPNPPPSP-PPSPPFPPAPPPSPPFPPTYKAKPTYKAKPTNPSTYKAKPSYPPTYKA 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09095443
                                                                                                                                                                                                                                                                                                 E: Lyon & Lyon
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                              Peles, Eior
IVENTION: DIAGNOSIS AND TREATMENT
IVENTION: OF ALP RELATED DISORDERS
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FastSEQ
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31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gregory
for Windows 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 226; DB 6
Pred. No. 7e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6; Length 334;
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                                                                                                                                                                                                          520236-37
520236-37
;Patent No. 5202236
;Patent No. 5202236
; Patent No. 5202236
; APPLICANT: MAUGH, KATHY J.;ANDERSON, DAVID M.;STRAUSBERG,
;SUSAN L.;MCCANDLISS, RUSS;WEI, TENA;FILPULA, DAVID
;MCCANDLISS, RUSS;WEI, TENA;FILPULA, RUSS;WEI, TENA;FILPULA, RUSS;WEI, RU
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                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.0
Best Local Similarity 29.8
Matches 115; Conservative
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                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/0 FILING DATE: June 12, 19 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   890 LSPYCPPLVATQAPLPGTA---ADFW 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      574 HHFSSGIPTGFPAPRIGPQPQPHPQPHPSQAFGPQ-----PPQQPLPLQHPHLFPPQAPG 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              629 LLPPQSPYP--YAPQPGVLGQPPP-PLHTQ--LYPGPAQDPLPAHSGALPFPSPGPPQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                       APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
                                                                                                                                     APPLICATION NUMBER: US/07/528,762 FILING DATE: 25-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QEHDARGRSIAIARCYSL-----KNRHQDVMPYDSNR----VVLRSGKDDYINASCVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----RGRTPSRHRSYERSRERERERHRHRD-----NRRSPSLERSYKKEYKRSGRSYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEGRRPQALRLIERDPYEH-----PERLRQLQQELEAFRGQLGDVGALDTVWRELQDA 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APSERRSPERLKHYDDHRHRDHSHGRGERHRSLDRR---ERGRSPDRRRQDSRYRSDYD- 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --PPAAE----PPPCLR-----RGAAAADLLSSSPESQHGGTQSPGGGQPLLQPTKVDA 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPPLAYGPAPSTRPMGPQAAPLTIRGPSSAGQSTPSPHLVPSPA-PSPGPGPVPPR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTFSNSPAPNFLPPRPDFVPFPPPMPPSAQGPLPPCPIRPPFPNHQMRHPFPVP-PCFPP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HRMSFHPGRGCPRGRGGHGARP-----SAPSFRPQNLRLLHPQQP-PVQYQY-EPPSAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSVVPEPAGCT-PELPGEIIKNTDSW 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1274 amino acids
NUMBER: 650,128
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US-09-041-886-23
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                                                                                                                                                    ; MOLECULE TYPE: protein US-09-041-886-23
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Patent No.
GENERAL IN
                                                                Query Match 2.9%; Score 220.5; DB 4; Best Local Similarity 21.5%; Pred. No. 1.2e-08; Matches 125; Conservative 29; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.0%; Score 225.5; DB 6; Best Local Similarity 31.2%; Pred. No. 7.5e-10; Matches 64; Conservative 13; Mismatches 85;
                                                                                                                                                                                                                                                                             TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bredesen, Date Per APPLICANT: Rabizadeh, Sharroz
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/041,886 FILING DATE: CLASSIFICATION:
ATTORNEY JACONTO.
                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1185 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 PSYPPTYKAKPSYP----PTYKAKP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 TYKAKP-SYPPTYKAKPSYPPTYKAKPTYKIKPTY-----PSTYKAKPTNPSTY--KAK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 NSSSPHFRHLPPYPLPKAPSERRSP 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 GQGTFPFMMPPPSMPHPPPPPPMPQQVNYQYPPGYSHHNFPPPSFNSFQNNPSSFLPSAN 197
14 PGRGC------PRGRG-GHGARPSAPSFRPQNLRLLH--------PQQPPVQYQYEP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 PPNPPPSPPPSPPFP------PAPPPSPPFPPTYKAKPTYKAKPTYKAKPTYKAKPSYPP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 AQGPLPPCPIRPPFPNHQMRHPFPVPPCFPPMPPPMPC-----PNNPPV----PGAPP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 PSAPSFRPQNLRLLHPQQPPVQYQYEPPSAPSTTFSNSPAPNFLPPRPDFVPFPPPMPPS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PPAPAFAPA-----PALAPAPPNPNPPSPPS-----PPSPPTPPPTPPSPPAPPSPPPS 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23, Application US/09041886
o. 6235872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Campbell & Flores LLP 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 331;
                                                                  Indels 279;
                                                                                                         Length 1185;
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                                                                Gaps
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** ** ** ** ** ** ** ** **		RESULT US-08 / Seque / Patel / GAN / AN / NI / NI	Qy Db	Db Qy	Qy Db	Оу	Qy Db	Qy Db	Qy Db	Qу	рь	ф
	A PER TAIL	SULT 8 -08-217-327-6 -08-217-327-6 -08-217-327-6 Sequence 6, Application US/08217327 Patent NO. 5474925 GEMERAL INFORMATION: ANIPAKAL E APPLICANT: John, Mallyakal E APPLICANT: John, Mallyakal E APPLICANT: Barton, Kenneth A TITLE OF INVENTION: Immobilized Proteins in Cotton Fiber NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS: ADDRESSEE: Quarles and Brady STREET: P.O. Box 2113 CITY: Madison	316 RSYGLSVVPEPAGCTPELPGEIIKNTDSWAPPLEIVNHRSP 356 	273RTPSRHRSYERSRERERERHRHRDNRRSPSLERSYKKEYKRSG 315	235 DHSHGRGERHRSLDRRERGRSPDRRRQDSRYRSDYDRG 272	186 QNNPSSFLPSANNSSSPHFRHLPPYPLPKAPSERRSPERLKHYDDHRHR 234	156PPPVMPQQVNYQYPPGYSHHNFPPPSFNSF 185	125 PCPNNPPVPGAPPGQGTFPFMMPPPSMPHPP	109MPPP	89AQGPLPPCP	56 PSAPSTTFSNSPAPNELPPRPDEVPEPPPMPPS	PGLGAQPLPGHLPSPYAMGQGMGGLPPGPEKGPTLAPSPHSLPPASSSAPAPPMRFPYSS

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US-08-574-959A-9
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US-08-574-959A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/08574959A Patent No. 5962224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Tocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                 NAME: Mandragouras, Amy E. REGISTATION NUMBER: 36,207
REFERENCATION NUMBER: DFI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi
APPLICANT: and Jack L. Strominger
TITLE OF INVENTION: 62 POLYPEPTIDES, RELATED POLYPEPTIDE
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                          FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 YKSPPPPKHSPAPVHHYKYKSPPPPTPVYKYKSPPPPKHSPAPEHHYKYKSPPPPKHFPA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94
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                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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                                  TOPOLOGY:
                                                               LENGTH:
                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                               amino acid
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                                                               905 amino acids
                                                                                                  (617)227-5941
(7) 17 NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 State Street,
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                                                                                                                                                                                                                                                                                               PatentIn Release #1.0,
                           linear
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              protein
                                                                                                                                                                                                                                              19-DEC-95
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                                                                                                                                                                         DFN-008
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Pred. No. 2.6e-09;
L4; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suite
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; Sequence 9, Application US/09357014
; Patent No. 6291645
; GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 FPPPMPPSAQ--GPLPPCPIRPPFPNHQMRHPFP------VPPCFPPMPPP 123
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                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/357,014
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi
and Jack L. Strominger
TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDE
                   PRIOR
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EETEDGSDKVQ-----PPPETPAEEEMETETEAEALQEKEQDDTAAMLAD 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EELGSRQEKAKAARPPWEPPKTKLDEDLESSSESEC--ESDEDSTCSSSSD 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKNEEEEEELLKPVWIRCTHSENYYSSDPMDQVGDSTVVGTSRLRDLYDK------FE 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IKNTDSWAPPLEIVNHRSPSREKKRARWEEEKDRWSDNQSSGKDKNYTSIKEKEPEETMP 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPERLKHYDDHRHRDHSHGRGERHRSLDRRERGRS---PDRRRQDSRYRSDYDRGRTPSR 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----XLPPPQLVP-EGTPGGGGPPALEEDLTVININSSDE------EEEE 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPSGATPP-PIAPTGP----PTASPPVPAKEEPEELPAAPGPLPPPPPPPPPPPVPGPV---- 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MPCPNNPPVPGAPPGQGTFPFMMPP------PSMPHPPPPPVMPQQVNYQY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAGPMPSAGPVPSEPWTSTTANLLGLLSRPSVCPPRLLPGPENHRAGSNEDPILAPSGTP 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SA-----PSTTFSNSPA-----PNFLPPR------PDFVP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCHRMSFHP-----GRGCPRGRGGHGARPSAPSFRPQN-LRLLHPQQPPVQYQYEPP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQGEVERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PPPESPPKVQPEPEPEPGLLLEVEEPGTE-EERGADTAPTL-----APEALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----EEEGELE-EEEEEEDEEEEEELEEVEDLEFGTAG-----GEVEEGAPPPPTLPPAL 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HRSYERSRERERHRHRDNRRSPSLERSYKKEYKRSGRSYGLSVVPEPAGCTPELPGEI 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -PPTIPPDETFGGRVP----RPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPP 567
                                       FILING DATE: 19-Jul-1999
                                                                                                                                                                                                                                                                       CITY: Boston
APPLICATION NUMBER: 08/574,959
                                                                                                                                                                                                          ZIP:
                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                   STATE: Massachusetts
                                                                                                                                                                                                                                                                                             STREET: 60 State Street,
                                                                                                                                                                                                                                                                                                                  ADDRESSEE: LAHIVE & COCKFIELD
                   APPLICATION DATA
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21.2%; Pred. No. 1.8e-08;
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                                                                                                                                                                                                                                                                                           Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GESPAAGPPP-QELVEEEPSXPPTLLE
                                                                                                      Version
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; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-357-014-9
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                                                                                                                                               Sequence 7, Application US/08574959A Patent No. 5962224
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                                                                                                                               GENERAL INFORMATION:
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TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 9:
               APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi APPLICANT: and Jack L. Strominger TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES TITLE OF INVENTION: AND USES THEREFOR NUMBER OF SEQUENCES: 22
CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169
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LENGTH: 905 amino acids
TYPE: amino acid
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ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPERLKHYDDHRHRDHSHGRGERHRSLDRRERGRS----PDRRRQDSRYRSDYDRGRTPSR 277
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                                                                                                                                                                                                                                                                                                                      EELGSRQEKAKAARPPWEPPKTKLDEDLESSSESEC--ESDEDSTCSSSSD 498
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Pred. No. 1.8e-08;
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                                                               RELATED POLYPEPTIDES
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Best Local Similarity
Matches 125; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION_DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: DF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/574,959A FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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CITY: Boston
STATE: Massac
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EFTEDGSDKVQ-----PPPETPAEEEMETETEAEALQEKEQDDTAAMLAD
                                                                                                           DKNEEEEEELLKPVWIRCTHSENYYSSDPMDQVGDSTVVGTSRLRDLYDK-----FE 449
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                                  EELGSRQEKAKAARPPWEPPKTKLDEDLESSSESEC--ESDEDSTCSSSSD 498
                                                                                                                                                -----pppesppkvqpepepepgllleveepgte-eergadtaptl-----apealp
                                                                                                                                                                                     IKNTDSWAPPLEIVNHRSPSREKKRARWEEEKDRWSDNQSSGKDKNYTSIKEKEPEETMP 397
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amino acid
DGY: linear
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(617)207-5941
(7) TO NO: 7:
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21.2%; Pred. No. 2.5e-08;
htive 58; Mismatches 212;
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RESULT 12
US-09-357-014-7
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; Patent No. 6291645
; Patent No. FORMATION:
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Local Similarity 21.2%;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAL PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/357,014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/574,959 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi and Jack L. Strominger
TITLE OF INVENTION: P62 POLYPEPTIDES, RELATED POLYPEPTIDES
AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1135 amino acids
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                                    SPERLKHYDDHRHRDHSHGRGERHRSLDRRERGRS---PDRRRQDSRYRSDYDRGRTPSR 277
                                                                                                                                                                                                                                             -PPTIPPDETFGGRVP----RPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPP
                                                                                                                    PPGYSHHNFPPPSFNSFQNNPSSFLPSA-----NNSSSPHFRHLPPYPLPKAPSERR 220
                                                                                                                                                             PPSGATPP-PIAPTGP---PTASPPVPAKEEPEELPAAPGPLPPPPPPPPPPPVPGPV----
                                                                                                                                                                                                      MPCPNNPPVPGAPPGQGTFPFMMPP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09357014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                             ---XLPPPQLVP-EGTPGGGGPPALEEDLTVININSSDE
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2%; Pred. No. 2.5e-08;
58; Mismatches 212; Indels 196; Gaps
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US-09-080-897-4
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Best Local
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                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Welcsh, Piri L.
APPLICANT: Leon, Pedro E.
TITLE OF INVENTION: Modulators
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: UW TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 343-4341
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ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
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MEDIUM TYPE: Floppy
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620 GACIPPPPQLPGSAAIPPPPPLPGVASIPPPPPLPGATAIPPPPPPLPGATAIP----PPPP 676
                                    114 PPCFPP------MPPPMPCPN-----NPPVPGAP------PGQGTFPFMMPPPS 150
                                                                          562 APSVSSSAAVPP--APPLEGDSGTVIPPPPPPPPPPPLPGGVVPPSPPLPPGTCIPPPPPLPG 619
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                                                   APSTTFSNSPAPNFLPPRP----DFVPFPPPMPPSAQGPLPPCPIRPPFPNHQMRHPFPV 113
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                                                                                                                                                           Similarity 32.1
63; Conservative
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Welcsh, Piri L.
Leon, Pedro E.
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                                                                                                                                                       2.7%; Score 203; DB 2; I
32.1%; Pred. No. 3.1e-07;
11. Mismatches 72;
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Sequence 1, Patent No.

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-
FILING DATE: 26-AUG-1996
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Narumiya, Shuh
APPLICANT: Takahashi, No. 6111072uaki
TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
TITLE OF INVENTION: ENCODING SAME
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
677 LPGGTGIPPPPPLPGSVGVPPPPPLPGGPGLPPP-----PPPFPGAPGIPPPPPGM 728
                                                                                                                                                 562 APSVSSSAAVPP--APPLPGDSGTVIPPPPPPPPPPPPPPSPPLPPGTCIPPPPPLPG 619
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                                                                        620 GACIPPPPQLPGSAAIPPPPPLPGVASIPPPPPLPGATAIPPPPPPLPGATAIP----PPPP 676
                                                                                                           114 PPCFPP-----MPPPMPCPN-----NPPVPGAP------PGQGTFPFMMPPPS 150
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                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                      58 APSTTFSNSPAPNFLPPRP----DFVPFPPPMPPSAQGPLPPCPIRPPFPNHQMRHPFPV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: JP 9-90170 FILING DATE: 25-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/899,595 FILING DATE: 24-JUL-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
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                                MPH----PPPPPVMPQQVNYQYPPGY-SHHNFPPPSFNSFQNNPSSFLPSANNSSSPHFR 205
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(202)672-5399
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ranatches 72;
                                                                                                                                                                                                                      11; Mismatches
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                                                                                                                                                                                                                                                          Length 1255;
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Best Local Similarity
Thes 63; Conserve
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US-09-323-735-4
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GENERAL INFORMATION:
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INFORMATION FOR SEQ
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Modulators of Actin NUMBER OF SEQUENCES: 14
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STATE: CALIFORNIA
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Search completed: October 9, 2002, 18:27:44
Job time: 46 secs

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APPLICANT: Brooksbank, Robert
APPLICANT: Pinnock, Robert
TITLE OF INVENTION: Identification and Use of
FILE REFERENCE: WI-A-018199
CURRENT APPLICATION NUMBER: US/10/205,331
CURRENT FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: GB 0118354.0
PRIOR APPLICATION NUMBER: GB 0118354.0
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 117
SOFTWARE: PATENTIN NOS: 117
SOFTWARE: PATENTIN VET. 2.1
SBO ID NO 116
LENGTH: 541
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US-10-205-331-116
; Sequence 116, Application US/10205331
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                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dixon, Alistair
                                      TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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PRIOR APPLICATION NUMBER: 60/217,486
PRIOR PILLING DATE: 2000-01-31
PRIOR PILLING DATE: 2000-02-04
PRIOR PILLING DATE: 2000-02-04
PRIOR PILLING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/2217,487
PRIOR PILLING DATE: 2000-07-11
PRIOR PILLING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILLING DATE: 2000-08-14
PRIOR PILLING DATE: 2000-07-26
PRIOR PILLING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: 60/221,496
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR APPLICATION NUMBER: 60/216,490
PRIOR FILLING DATE: 2000-08-14
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Best Local S
Matches 537
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TITLE OF INVENTION: Nuc
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Pred. No. 2.8e
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PRIOR APPLICATION NUMBER: 60/ PRIOR FILING DATE: 2000-09-05 PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR FILING DATE: 2000-09-08 PRIOR FILING DATE: 2000-09-05 PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR FILING DATE: 2000-09-29 PRIOR APPLICATION NUMBER: 60/	APPLICATION NUMBER: FILING DATE: 2000-1 APPLICATION NUMBER: FILING DATE: 2000-1 APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2000-1 APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2000-0	APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2000-1 APPLICATION NUMBER: FILING DATE: 2000-1 APPLICATION NUMBER: FILING DATE: 2000-1 APPLICATION NUMBER: FILING DATE: 2000-1 APPLICATION NUMBER: FILING DATE: 2000-1 APPLICATION NUMBER: FILING DATE: 2000-1 APPLICATION NUMBER: FILING DATE: 2000-1 APPLICATION NUMBER: FILING DATE: 2000-1	APPLICATION NUMBER: FILING DATE: 2000-08 APPLICATION NUMBER: FILING DATE: 2000-08 APPLICATION NUMBER: FILING DATE: 2000-07 APPLICATION NUMBER: FILING DATE: 2000-09 APPLICATION NUMBER: FILING DATE: 2000-09 APPLICATION NUMBER: FILING DATE: 2000-09 APPLICATION NUMBER: FILING DATE: 2000-09 APPLICATION NUMBER: FILING DATE: 2000-09 APPLICATION NUMBER: FILING DATE: 2000-09
60/229,513 9-05 60/231,413 9-08 60/229,509 9-05 60/236,367 9-29 60/237,039 0-02 60/237,038 0-02 60/237,038 0-02 60/236,370 9-09	241, 244, 225, 236, 251, 251, 229, 229, 229, 229, 229,	4, 27 4, 22 18, 92 16, 36 16, 36 11, 80 11, 80	225, 226, 216, 225, 225, 225, 225, 235,
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PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,040
PRIOR APPLICATION NUMBER: 60/240,960
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/249,935
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/239,937
PRIOR APPLICATION NUMBER: 60/249,937
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PRIOR APPLICATION NUMBER: 60/249,216
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PRIOR APPLICATION NUMBER: 60/249,216
PRIOR APPLICATION NUMBER: 60/249,216
PRIOR APPLICATION NUMBER: 60/225,759
PRIOR PILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/225,216
PRIOR APPLICATION NUMBER: 60/225,216
PRIOR APPLICATION NUMBER: 60/225,216
PRIOR APPLICATION NUMBER: 60/225,216
PRIOR APPLICATION NUMBER: 60/225,216
PRIOR APPLICATION NUMBER: 60/225,216
PRIOR APPLICATION NUMBER: 60/225,216
PRIOR APPLICATION NUMBER: 60/235,836
PRIOR FILING DATE: 2000-08-12
PRIOR APPLICATION NUMBER: 60/235,836
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/249,213
PRIOR APPLICATION NUMBER: 60/249,213
PRIOR APPLICATION NUMBER: 60/249,213
PRIOR APPLICATION NUMBER: 60/249,213
PRIOR APPLICATION NUMBER: 60/249,213
PRIOR APPLICATION NUMBER: 60/249,213
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PRIOR APPLICATION NUMBER: 60/249,217
PRIOR APPLICATION NUMBE

APPLICATION FILING DATE:

NUMBER:

60/231,414

2000-09-08

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US-10-103-313-471

Sequence 471, Application US/10103313

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, an
FILE REFERENCE: PUZ07C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
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R APPLICATION NUMBER: 60/241,808
OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/241,826
OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/241,786
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FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/232,397
FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/232,399
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APPLICATION NUMBER: 60/246,475
FILING DATE: 2000-11-08
APPLICATION NUMBER: 60/231,243
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APPLICATION NUMBER: 60/232,401
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FILING DATE: 2000-09-14
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Pred. No. 1.8e-85;
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APPLICATION NUMBER: 60/225,447
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/218,290
FILING DATE: 2000-07-14
APPLICATION NUMBER: 60/225,757
FILING DATE: 2000-08-14

APPLICATION NUMBER: 60/226,868

2000-08-22

FILING DATE APPLICATION

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US-09-764-882A-377; Sequence 377, Applicatio; GENERAL INFORMATION:
APPLICANT: Rosen et al.
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR PPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR PILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR PRIOR DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR PRIOR FILING DATE: 2000-07-11
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Matches 374;
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Best Local
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Pred. No. 1
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PRIOR APPLICATION NUMBER: 60/235,35/ PRIOR EILING DATE: 2000-09-29 PRIOR APPLICATION NUMBER: 60/237,039 PRIOR APPLICATION NUMBER: 60/237,039 PRIOR APPLICATION NUMBER: 60/237,038 PRIOR PILING DATE: 2000-10-02 PRIOR APPLICATION NUMBER: 60/236,370 PRIOR PILING DATE: 2000-09-29 PRIOR APPLICATION NUMBER: 60/236,802 PRIOR FILING DATE: 2000-10-02 PRIOR FILING DATE: 2000-10-02 PRIOR FILING DATE: 2000-10-02 PRIOR APPLICATION NUMBER: 60/237,037 PRIOR APPLICATION NUMBER: 60/237,037 PRIOR APPLICATION NUMBER: 60/237,040 PRIOR APPLICATION NUMBER: 60/237,040 PRIOR PILING DATE: 2000-10-02	FILING DATE: 2000-09-25 APPLICATION NUMBER: 60/229, FILING DATE: 2000-09-01 APPLICATION NUMBER: 60/229, FILING DATE: 2000-09-01 APPLICATION NUMBER: 60/229, FILING DATE: 2000-09-01 APPLICATION NUMBER: 60/229, FILING DATE: 2000-09-05 APPLICATION NUMBER: 60/229, FILING DATE: 2000-09-05 APPLICATION NUMBER: 60/229, FILING DATE: 2000-09-05 APPLICATION NUMBER: 60/221, FILING DATE: 2000-09-05 FILING DATE: 2000-09-05 APPLICATION NUMBER: 60/229, FILING DATE: 2000-09-05	FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/236, FILING DATE: 2000-09-29 APPLICATION NUMBER: 60/241, FILING DATE: 2000-10-20 APPLICATION NUMBER: 60/241, FILING DATE: 2000-11-01 APPLICATION NUMBER: 60/225, FILING DATE: 2000-08-14 APPLICATION NUMBER: 60/236, FILING DATE: 2000-09-29 APPLICATION NUMBER: 60/251, FILING DATE: 2000-12-08 APPLICATION NUMBER: 60/251, FILING DATE: 2000-12-08 APPLICATION NUMBER: 60/251, FILING DATE: 2000-12-08 APPLICATION NUMBER: 60/251, FILING DATE: 2000-12-08 APPLICATION NUMBER: 60/229, APPLICATION NUMBER: 60/234 APPLICATION NUMBER: 60/234	R APPLICATION N R FILING DATE: R APPLICATION N	FILING DATE: 2000-07-07 APPLICATION NUMBER: 60/225, FILING DATE: 2000-08-14 APPLICATION NUMBER: 60/216, FILING DATE: 2000-07-07 APPLICATION NUMBER: 60/225, FILING DATE: 2000-08-14 APPLICATION NUMBER: 60/251, FILING DATE: 2000-12-08 APPLICATION NUMBER: 60/235, APPLICATION NUMBER: 60/234, FILING DATE: 2000-09-27 APPLICATION NUMBER: 60/234, FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-14 PRIOR APPLICATION NUMBER: 60/231,242 PRIOR APPLICATION NUMBER: 60/231,242 PRIOR APPLICATION NUMBER: 60/231,242 PRIOR APPLICATION NUMBER: 60/232,081 PRIOR APPLICATION NUMBER: 60/232,081 PRIOR APPLICATION NUMBER: 60/232,080 PRIOR FILING DATE: 2000-09-08 PRIOR FILING DATE: 2000-09-08 PRIOR FILING DATE: 2000-09-08 PRIOR APPLICATION NUMBER: 60/231,414 PRIOR APPLICATION NUMBER: 60/231,244 PRIOR FILING DATE: 2000-09-08 PRIOR APPLICATION NUMBER: 60/231,244 PRIOR FILING DATE: 2000-09-08 PRIOR APPLICATION NUMBER: 60/231,064	APPLICATION N FILING DATE: APPLICATION N FILING DATE: APPLICATION N FILING DATE: APPLICATION N FILING DATE: APPLICATION OF FILING DATE: APPLICATION OF FILING DATE: APPLICATION OF FILING DATE: APPLICATION OF APPLICATI	PRIOR APPLICATION NUMBER: 60/230,438 PRIOR FILING DATE: 2000-09-06 PRIOR APPLICATION NUMBER: 60/215,135 PRIOR APPLICATION NUMBER: 60/225,266 PRIOR APPLICATION NUMBER: 60/249,218 PRIOR APPLICATION NUMBER: 60/249,218 PRIOR FILING DATE: 2000-01-17 PRIOR FILING DATE: 2000-11-17 PRIOR APPLICATION NUMBER: 60/249,213 PRIOR FILING DATE: 2000-11-17 PRIOR APPLICATION NUMBER: 60/249,217 PRIOR FILING DATE: 2000-11-17 PRIOR APPLICATION NUMBER: 60/249,207 PRIOR FILING DATE: 2000-11-17 PRIOR APPLICATION NUMBER: 60/249,245 PRIOR FILING DATE: 2000-11-17	FILING DATE: 2000-11 APPLICATION NUMBER: FILING DATE: 2000-12 APPLICATION NUMBER: FILING DATE: 2000-06 APPLICATION NUMBER: FILING DATE: 2000-06 APPLICATION NUMBER: FILING DATE: 2000-08 APPLICATION NUMBER: FILING DATE: 2000-08 APPLICATION NUMBER: FILING DATE: 2000-08 APPLICATION NUMBER: FILING DATE: 2000-08 APPLICATION NUMBER: FILING DATE: 2000-08 APPLICATION NUMBER: FILING DATE: 2000-08 APPLICATION NUMBER:	APPLICATION N FILLING DATE: APPLICATION N FILLING DATE: APPLICATION N FILLING DATE: APPLICATION N FILLING DATE: APPLICATION N FILLING DATE: APPLICATION N FILLING DATE: APPLICATION N FILLING DATE: APPLICATION N

DR FILLING DATE: 2000-08-22

PR APPLICATION NUMBER: 60/225,759

PR APPLICATION NUMBER: 60/225,213

PR FILLING DATE: 2000-08-14

PR APPLICATION NUMBER: 60/227,182

PR FILLING DATE: 2000-08-22

PR FILLING DATE: 2000-08-22

PR FILLING DATE: 2000-08-24

PR FILLING DATE: 2000-09-27

PR FILLING DATE: 2000-09-27

PR FILLING DATE: 2000-09-27

PR FILLING DATE: 2000-09-26

PR FILLING DATE: 2000-09-27

PR FILLING DATE: 2000-09-27

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PR FILLING DATE: 2000-09-27

PR FILLING DATE: 2000-08-14

PR FILLING DATE: 2000-08-14

PR FILLING DATE: 2000-11-17

PR APPLICATION NUMBER: 60/249,213

PR FILLING DATE: 2000-11-17

PR APPLICATION NUMBER: 60/249,213

PR APPLICATION NUMBER: 60/249,213

PR PR FILLING DATE: 2000-11-17

PR APPLICATION NUMBER: 60/249,212

PR FILLING DATE: 2000-11-17

PR APPLICATION NUMBER: 60/249,213

PR APPLICATION NUMBER: 60/249,217

PR APPLICATION NUMBER: 60/249,217

PR APPLICATION NUMBER: 60/249,244

PR FILLING DATE: 2000-11-17

PR APPLICATION NUMBER: 60/249,217

PR APPLICATION NUMBER: 60/249,217

PR APPLICATION NUMBER: 60/249,217

PR APPLICATION NUMBER: 60/249,217 DR APPLICATION NUMBER: 60/240,960
RR FILING DATE: 2000-10-20
RR APPLICATION NUMBER: 60/239,935
RR FILING DATE: 2000-10-13
RR APPLICATION NUMBER: 60/239,937
RR APPLICATION NUMBER: 60/241,787
RR FILING DATE: 2000-10-20
RR FILING DATE: 2000-10-20
RR APPLICATION NUMBER: 60/246,474
RR FILING DATE: 2000-11-08
RR FILING DATE: 2000-11-08
RR FILING DATE: 2000-11-08
RR FILING DATE: 2000-11-08
RR FILING DATE: 2000-11-08
RR FILING DATE: 2000-11-08
RR FILING DATE: 2000-11-08 APPLICATION NUMBER: 60/249,216 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,210 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/226,681

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US-10-103-313-307; Sequence 307, Application US/10103313; GENERAL INFORMATION:
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                APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodi.
TITLE REFERENCE: PJZ07C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 307
SEQ ID NO 307
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Best Local Similarity
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TYPE: PRT
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OR FILING DATE: 2000-10-20
OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/241,786
OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/241,221
OR APPLICATION NUMBER: 60/246,475
OR FILING DATE: 2000-11-08
OR APPLICATION NUMBER: 60/231,243
OR APPLICATION NUMBER: 60/231,243
OR APPLICATION NUMBER: 60/233,065
OR FILING DATE: 2000-09-18
OR APPLICATION NUMBER: 60/233,065
OR FILING DATE: 2000-09-14
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OR APPLICATION NUMBER: 60/233,063
OR FILING DATE: 2000-09-14
OR APPLICATION NUMBER: 60/232,397
OR FILING DATE: 2000-09-14
OR APPLICATION NUMBER: 60/232,399
OR FILING DATE: 2000-09-14
OR APPLICATION NUMBER: 60/232,401
OR APPLICATION NUMBER: 60/232,401
OR APPLICATION NUMBER: 60/241,808
OR APPLICATION NUMBER: 60/241,808
OR FILING DATE: 2000-10-20
OR FILING DATE: 2000-10-20
OR FILING DATE: 2000-10-20
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98.7%;
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Pred. No. 3.1e-85
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PRIOR EPLICATION NUMBER: US 08/905,223
PRIOR APPLICATION NUMBER: US 08/905,135
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,135
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,051
PRIOR APPLICATION NUMBER: US 08/905,144
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,279
PRIOR APPLICATION NUMBER: US 08/905,279
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/904,468
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,134
PRIOR APPLICATION NUMBER: US 08/905,134
PRIOR APPLICATION NUMBER: US 08/905,133
PRIOR APPLICATION NUMBER: US 08/905,133
PRIOR FILING DATE: 1997-08-01
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SEQ ID NO 3281
LENGTH: 115
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dumas Milne Edwards, Jean Baptiste APPLICANT: Duclert, Aymeric APPLICANT: Lacroix, Bruno
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 3475
                                                          LOCATION: -23..-1
OTHER INFORMATION:
OTHER INFORMATION:
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FEATURE:
                  OTHER INFORMATION:
                                         FEATURE:
                                                                                                                                  NAME/KEY: SIGNAL
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Lacroix, Bruno
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                  seq TLKFLTLLQKSNA/KR
                                                              score 5.
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Pred. No. 2.9e-55;
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RESULT 9
US-09-791-537-62108
; Sequence 62108, Application US/09791537
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 130915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Blonomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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     APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
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CURRENT FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     watch 4.2%; Score 315; DB 5; Length 249; Local Similarity 34.7%; Pred. No. 1.2e-07; Nes 85; Conservative 46; Mismatches 96; Indels
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Similarity 95.7%;
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2001-02-22
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; TYPE: PRT ; ORGANISM: Bacillus subtilis US-09-791-537-104336
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SOFTWARE: PatentIn version 3
SEQ ID NO 62108
LENCTH: 266
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.0 SEQ ID NO 104336 LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 4.1%;
Best Local Similarity 34.2%;
Matches 83; Conservative 4
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Best Local :
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THERBOF
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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                                         EPDIPLYKTLQTVGPSHARTYTVAVYFKGERIGCGKGPSIQQAEMGAAMDA---LEKYNF 1334
                                                                                                                                            LESFIAALYTDKDLEYVHTFMNVCFFPRLKEFILNQDWNDPKSQLQQCCLTLRTEGK--- 1277
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E----YKISNEKGPAHNREFEAIVSLKGEPLGVGNGRSKKEAEQHAAQEALAKLEKHHT
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                                                                                                FKAFIGALYLDQGLEPVESFLKVYVFPKINDGAFPHVM-DFKSQLQE---YVQRDGKGSL
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Pred. No. 3.8e-07;
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US-10-216-583-1603
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CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 09/760,469
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR APPLICATION NUMBER: 60/214,487
PRIOR FILING DATE: 2000-06-28
PRIOR PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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NUMBER OF SEQ ID NOS: 1983
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1603
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PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
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OTHER INFORMATION: Xaa
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TYPE: PRT
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LOCATION: (189)
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MPHPPP--PPVMPQQVMYQYPPGYSHHNFPPPSFNSFQNNPSSFLPSANNSSSP---HFR :| | | | | : | :| : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : | : : : : | : : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : : | : : : : | : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : : | : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : | : : : : : | : : : : | : : : : | : :
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27.2%;
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US-09-935-625-17077
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Best Local Similarity
Matches 158; Conserv
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CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 17077
LENGTH: 827
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNICLEOTIDES, POLYPEPTIDES,
TITLE OF INVENTION: MODULATING VARIOUS RESPONSES
FILE REFERENCE: 2750-1481P
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                                     GRKHQRERRSPGRLSEEQDRVQNSKLLKRTSVPDTDKRKQLPEKLLEVGRVEHYKEQERK 642
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LLKPVWIRCTHSENYYSSDPMDQVGDSTVVGTSRLRDLYDKFEEELGS-
                                                                        EKKRARWEEEKDRWSDNQ---SSGKDKNYTSIKEKEPEETMPDK-----
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Pred. No. 4.5e-05;
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; LCCATION: 1.847
; OTHER INFORMATION: Ceres Seq.
US-09-935-625-17076
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CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 17076
LENGTH: 847
TYPE: PRT
ORGANISM: Arabidopsis thaliana
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
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                                                            GRKHQRERRSPGRLSEEQDRVQNSKLLKRTSVPDTDKRKQLPEKLLEVGRVEHYKEQERK
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          SDKLSEKRSVHRHHGSQMSPVENSEGRSRPVSSKVKD-SEQVEKEDNSDLDANLSCDSKD
                                    LLKPVWIRCTHSENYYSSDPMDQVGDSTVVGTSRLRDLYDKFEEELGS--------
                                                                                                                                                                  RGKSSPS-SRHQKARSPVRRRSP---
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; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..859
; OTHER INFORMATION: Cere
US-09-935-625-17480
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US-09-935-625-17480
US-09-935-625-17480
Sequence 17480, Application US/09935625
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CEITITLE OF INVENTION: MODDLATING VARIOUS RESPONSES
FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 17480
LENGTH: 859
TYPE: PRT
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---ROEKAKAARPPWEPPKTKLDEDLESSSESECESDEDSTCSSSSDSEVFDVIAEIKRK 511
                                                 SDKLSEKRSVHRHHGSQMSPVENSEGRSRPVSSKVKD-SEQVEKEDNSDLDANLSCDSKD
                                                                                               LLKPVWIRCTHSENYYSSDPMDQVGDSTVVGTSRLRDLYDKFEEELGS--
                                                                                                                                                                                               EKKRARWEEEKDRWSDNQ---SSGKDKNYTSIKEKEPEETMPDK-----NEEEEEE
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Sequence 17479, Application US/09935625 Sequence 17479, Application US/09935625 Sequence 17479, Application US/09935625 Sequence 17479, Application US/09935625 Sequence 17479 APPLICANT: N. ALEXANDROY et al. TITLE OF INVENTION: MODILATING VARIOUS RESPONSES FILE REFERENCE: 2750-1481 CURRENT FILING DATE: 2001-08-24 NUMBER OF SEQ ID NO. 17479 SEQ ID NO. 17479 SEQ ID NO. 17479 ORGANISM: ARABIGOPSIS thaliana FRATURE: NAME/KEY: Peptide LOCATION: 1.879 OPEN: NFT ORGANISM: ARABIGOPSIS thaliana FRATURE: SEG ID NO. 17479 OUGHEN IMPORMATION: Ceres Seq. ID NO. 3023745 OPEN: IMPORMATION: Ceres Seq. ID NO. 3023745 OPEN: NFT ORGANISM: ARABIGOPSIS THALIANA FRATURE: SEG ID NO. 17479 OUGHEN IMPORMATION: Ceres Seq. ID NO. 3023745 OPEN: NFT ORGANISM: ARABIGOPSIS THALIANA FRATURE: 1	Qy 512 KAHPDRLHDELWYNDPGQMNDGPLCKCSAKARRTGIRH 549 :
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Search completed: October 9, 2002, 18:35:10 Job time : 206 secs

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ALIGNMENTS

C;Date: 13-000 P. C;Accession: T21419
C;Accession: T21419
R;Lightning, J.
submitted to the EMBL Data Library,
submitted to number: Z19419 hypothetical protein F26E4.13 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type; DNA
A;Molecule type; DNA
A;Residues: 1-412 <MIL>
A;Cross-references: EMBL:Z81070; PIDN:CAB03005.1; GSPDB:GN00019; CESP:F26E4.13
A;Experimental source: clone F26E4
C;Genetics: Constant δÃ Ωy 2 Q δÃ 밁 Qy Вb 밁 QY 망 밁 Вb A; Map position: 1 A; Introns: 359/2; 400/3 A; Gene: CESP:F26E4.13 A; Reference number: A; Accession: T21419 Query Match Best Local Similarity Matches 1183 1123 1064 FGRLLF-NDPDLREVWLNYPLHPLQLQEPNTDRQLIETSPVLQKLTEFEEAIGVIFTHVR 1122 1299 TVAVYFKGERIGCGKGPSIQQAEMGA---AMDALEKYNFPQM-AHQKRFIGRKYRQELKE 1354 1004 VQNQHLAMLAKKLELDPFMLYAHGPDLCRESDLRHAMANCFEALIGAVYLEGSLEEAKQL 1063 118 944 TLINIMSRLGQDDPTPSRINHNERLEFLGDAVVEFLTSVHLYYLFPSLEEGGLATYRTAI 1003 58 2 SLFNIMKGTSGGEP----ILHNERLEYLGDAVVELIVSHHLYFMLTHHFEGGLATYRTAL 57 LLARAFTLRTVGFNHLTLGHNQRMEFLGDSIMQLVATEYLFIHFPDHHEGHLTLLRSSLV 1182 KIAVYYKGKRLASAAESNVHKAELRVAELALANLESMSFSKMKAKNNSNMRRRLEQDTSD 412 FMNVCFFPRLKEFILNQDWNDPKSQLQQCCLTLR-TEGKEPDIPLYKTLQTVGPSHARTY 1298 VQNRNLATLAKNCRIDEMLQYSHGADLINVAEFKHALANAFEAVMAAIYLDGGLAPCDVI 117 FSKAMYGHQPVLKEKWDHINEHELKREDPQGDRDLSFITPTLSTFHALEERLGIQFNNIR 177 181; Conservative 11.9%; Score 890; DB 2 43.1%; Pred. No. 3e-40; 85; Mismatches 136; Indels October 1996 , د Length 412 18; Gaps

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C:Species: Laure | Sequence C:Date: 15-Oct-1999 #sequence C:Accession: T21420 R:Lightning, J. submitted to the EMBL Data L. Su
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A; Introns: 119/3; 226/2;
C; Superfamily: Caenorhab
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKEVLSMHQILLYLL-RCSKALVPEEEIANMLQWEELEWQKYAEECKGMIVTNPGTKPSS 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSPPTNFLTDRPTVIEYDDHEYIFEGFSMFAHAPL----TNIPLCKVIRFNIDYTIHFIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DELWYNDPGQMNDGPLCKCSAKARRTGIRHSIYPGEEAIKPCRPMTNNAGRLFHY--RIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEDLESSSESECESDEDSTCS------SSSDSEVFDVIAEIKRKKAHPDRLH 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIIKNTDS-----WAPPLEIVNHRSPSREKKRARWEEEKDRWSDNQSSGKDKNYTSIK 388
YNFSLDVFEEVIEYKFNDRRVIELALMHSSFKSHYGTPIDHVKNMITNCGYRR-KYG---
                                                             YHQCLMHLDKLIGYTFQDRCLLQLAMTHPSHHLNFGMNPDHARNSLSNCGIRQPKYGDRK 931
                                                                                                                                                                                                   QTDKQKLAQREEALQKIRQKNTMRREVTVELSSQGFWKTGIRSDVCQHAMMLPVLTHHIR 871
                                                                                                                                                                                                                                                                           IRADWFERDEEKKEV----YVVHNAIRAQTYTAISLPRIAFLEKTLNKMIQ-EKQSSGVY
                                                                                                                                                                                                                                                                                                                                                                                                                 LVQLWSSKTVLAYFTSKGSSEIMSPEDVNRLCDAQIDQFTRNTSKHKQSIVLNTKFKPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFMPDECFDPEDCDMLFEYIFHEIFEMLDFELRPKHIPSDVESCPMIHIMPRFVQ-TKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GE------VKDEKQTCNRRNQQRKAKRLRNFEEKERQITLLKKGIDRKKTHPNGIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGDESFTASDVSDDSNDS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEEAEKYMMIKAKSTTSKILQDFQTKILETVKTKRRLQADVPYIIHPCHSMKGRKTPKQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSPRLTEKDYETNYMIDPP--VVSTHSAELIK---
                                                                                                                                     NKDFEK---TKNELEHLKRENRSARNLKLREPVAGFIETGLKPDVAAHVVMTILACHHIR
                                                                                                                                                                                                                                                                                                                                            VRIDQLDREQFNPDVITFPIIVHFGIRPAQLSYAGDPQYQKLWKSYVKLRHLLANSPKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLPSENQL--YRTHMAINGEEFEFEGFSLITHAPLPDCMTRAPICK---YSMDYEFQLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDISFNEKGLGNEGPECRCPEPIKTCGLKHGYYAGEDKAIDCK--KSNGENLHYYTLRVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---ENYYSSDPMDQVGDSTVVGTSRLRDLYDKFEEELGSRQEKAKAARPP--WEPPKTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KHKRARRKKYQKEYQERHKEEMMQQLGRRFQNQPSTSSAPPDTVEKIPLPTESTSALPFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.4%; Score 558; DB 2; Lilarity 24.1%; Pred. No. 2.7e-22; Conservative 126; Mismatches 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303/2; 377/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -QDEASTSEPTNRQAPEADKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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N;Alternate names: HPBRII-4 protein C;Species: Homo sapiens (man) C;Date: 10-Oct-1995 #sequence_revision C;Accession: S57447; S57489
                                                                                            Qγ
                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: unassigned ribonucleoprotein repeat- F; 82-151/Domain: ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data A; Reference number: S57447 A; Accession: S57447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-551 <FLE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-551 <FL2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S57489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Fleischhauer, K.L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPBRII-7 protein
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 515
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                       SRHRSYERSRERERHRHRDNRRSPSLERSYKKEYK 312
DRHDDYYRERSRERERHRDRD--RDRDRERDREREYR
                                                                                                                                                            PLPKAPSERRSPERLKHYDDHRHRDHS-----
                                                                                                                                                                                                                                                                                                                                                                                                                   PRGRGGHGARPSAPSFRPQNLRLLHPQQPPVQYQYEPPSAPSTTFSNSPAPNF----LPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary
                                                                                                                                                                                                              MPQQVNYQYPPGYSHHNFPPPSFNSFQNNPSSFLPSANNSSSP---HFRHLPPY-----
                                                                                                                                                                                                                                                        GPPP-PVPGYGPPPGPPPPQQGPPPPPGPFPPRPPGPLGPPLTLAPPPHLPGPPPGAPPP
                                                                                                                                                                                                                                                                                       MPPPMPCPNNPPVPGAPPGQ------GTFP-----FMMPPPSMPHPPP--PPV 159
                                                              QSKVSADDRCKVLISSLQDCLHGIESKSYGSGSRRERSRERDHSR--SREKSRRHKSRSR
                                                                                                                            PPGREMDTARTPLSEAEFEEIMNRNRAISSSAISRAVSDASAGDYGSAIETLVTAISLIK
                                                                                                                                                                                          AP-HVN----PAF----FPPPT-----NSGMPTSDSRGPPPTDPYGRPPPYDRGDYG
                                                                                                                                                                                                                                                                                                                                                     RPDFVPFPPPMPPSAQGPLPPCPIRPP----FPNHQMRHPFPV------PPC--FPP 119
                                                                                                                                                                                                                                                                                                                     RP---PLGPPGPPGPPPPPGQVLPPPLAGPPNRGDRPPPPVLFPGQPFGQPPLGPLPP
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HPBRII-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL:x67336; NID:g871300;
                                                                                          ------HG-RGERHRSLDRRERGRSPDRRRQDSRYRSDYDRGRTP 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 316; DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     -VPGGDRFPGPAGP----GGPPPPFPAGQTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-Nov-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN:CAA47752.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDN:CAA47751.1;
 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <RRM4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   148;
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ribonuclease III (EC 3.1.26.3) - Bacillus subtilis
N;Alternate names: RNase D; RNase O
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
C;Accession: B6993; JC4821
R;Kunst, F; Ogsaswara, N; Moszer, I.; Albertini, A.M.; Alloni,
C;;Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuan

Albertini, A.M.; Alloni, V.; Caldwell, B.; Capuano

Capuano,

. G.; . V.;

Carter,

V.; Ber , N.M.;

20-Jun-2000 Azevedo,

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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallex lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A,Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot Reuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Reference number: A69580; MUID:98044033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Oguro, A.; Kakeshita, H.; Takamatsu, H.; Nakamura, K.; Yamane, K. Gene 17, 17-24, 1996
A:Title: The effect of Srb, a homologue of the mammalian SRP receptor alpha-subunit, A:Reference number: JC4819; MUID:96257247
                                                                                                                  ribonuclease III homolog rncS [imported] - Listeria monocytogenes (strain EGD-C;Specles: Listeria monocytogenes C;Specles: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C;Accession: AE1300 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: ribonuclease III; double-stranded RNA-binding repeat C;Kcywords: hydrolase F;172-245/Domain: double-stranded RNA-binding repeat homology <DSR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
A;Gene: rncS; srb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-78,'p',80-137,'K',139-170,'p',172-242,'E',244-249,'ENPPYDSGGFQYVCRLI'
A; Cross-references: DDBJ:D64116; NID:g1389548
A; Cross-references: DBJ:D64116; NID:g1389548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-249 <KUN>
A; Cross-references: GB:Z99112; GB:AL009126; NID:g2633902;
A; Experimental source: strain 168
               Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.;
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A;Status: nucleic acid sequence not shown; translation not shown
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Nature 390, 249-256,
  ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; V. A;Title: Comparative genomics of Listeria species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                   Jones, L.M.; Karst,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1104 LQKLTEFEEAIGVIFTHVRLLARAFTLRTVGFNHLTLGH--NQRMEFLGDSIMQLVATEY 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137
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                                                                                                                                                                                                                                                                                                                                                                                     HHTKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                    AHQKR 1342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPDIPLYKTLQTVGPSHARTYTVAVYFKGERIGCGKGPSIQQAEMGAAMDALEKYNFPQM 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEAFIGALYLDQGLEPVESFLKVYVFPKINDGAFSHVM-DFKSQLQE---YVQRDGKGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LESFIAALYTDKDLEYVHTFMNVCFFPRLKEFILNQDWNDPKSQLQQCCLTLRTEGK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFAKYPAMSEGDLTKLRAAIVCEPSLVSLAHELSFGDLVLLGKGEEMTGGRKRPALLADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEQFKEFQERISVHFQNEKLLYQAFTHSSYVNEHRKKPYEDNERLEFLGDAVLELTISRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YKISNEKGPAHNREFEAIVSLKGEPLGVGNGRSKKEAEQHAAQEALAKL---QK
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                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.2%; Score 315; DB 2; 34.7%; Pred. No. 6.8e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry
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                          Maitournam, A.;
Voss, H.; Wehla
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                                                                                                                , P.;
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                                                                                                                          ; Bloecker
Fsihi, H.
                            Wehland
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A;Accession: AE1300
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-229 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: rncS
C;Superfamily: ribonuclease III; double-stranded RNA-binding repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: rncs
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AE1672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-229 <GLA>
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A;Experimental source: strain EGD-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ribonuclease III homolog rncs [imported] - Listeria
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                                                                                                                                                                                                                                                                               1109 EFEEAIGVIFTHVRLLARAFTLRTVGFNHL--TLGHNQRWEFLGDSIMQLVATEYLFIHF 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1109 EFEEAIGVIFTHVRLLARAFTLRTVGFNHL--TLGHNQRWEFLGDSIMQLVATEYLFIHF 1166
  1283 L-YKTLQTVGPSHARTYTVAVYFKGERIGCGKGPSIQQAEMGAAMDALEKYNFPQMAHQ 1340
                                                      125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IEYDILGETGPAHNKAFDAQVIVNGQVLGKGSGRTKKQAEQSAAQFAINK
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                                                    IGALYLDNGIDKVVKFLERVIFPKIDAGAYLQTVDY----KTQLQEIV-----QRDRDVL 175
                                                                                                                                                         PDMAEGHMTKMRAAIVCEPSLVEFAEAVHFSKY-VRLGKGEEKAGGRTRPALLADVFESF 124
                                                                                                                                                                                                        PDHHEGHLTLLRSSLVNNRTQAKVAEELGMQEYAITNDKTKRPVGLRTK--TLADLLESF 1224
                                                                                                                                                                                                                                                       ELQESVGFDFQNVELLQQAFTHSSYVNEHRRENVKDNERLEFLGDAVLELTVSDYLFNKY 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGALYLDNGIDKVVTFLERVIFPKIDAGAYLQTVDY---KTQLQEIV-----QRDRDVL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDMAEGHMTKMRAAIVCEPSLVEFAEAVHFSKY-VRLGKGEEKAGGRTRPALLADVFESF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELQESVGFDFKNVELLKQAFTHSSYVNEHRRENVKDNERLEFLGDAVLELTVSDYLFNKY
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Similarity 33.0%;
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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31.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 307.5;
Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                                                                  Score 300; DB 2;
Pred. No. 3.8e-09;
                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 229
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urget, O.; Entian,
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Voss, H.; Wehla
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; Bloec Fsihi,

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K; Witte, M.M.; Scott, R.E.
submitted to the EMBL Data Library, November 1998
A; Reference number: Z22246
A; Accession: T42727
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: I-1560 <WIT>
A; Cross-references: EMBL:U83913; NID:g3858884; PID:g3858885; PIDN:AAC72432.1
A; Experimental source: Strain Balb/C
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: P2P-R
C;Function:
A;Description: in:
C;Superfamily: RI
F;57-107/Domain:
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c;SpecLes: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 02-Sep-2000
C;Accession: T42727
R;Witte, M.M.; Scott, R.E.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
 KEEATKIDSVKPSSSSQKDEKVTGT
                                                                                                                                                                                                                SHRNRNLGGNYPEKLSTRDSHNAKDNPKSKEKESENVPGDGKGNKHKKHRKRRNEEKGEE
                                                                                                                                                                                                                                                                                                                                                                                                   RHRSYERSRERERER-HRHR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQPPTAG---YSVPPPGFPPAPANISTACFSPGVPTAHSNTMPTTQAPLLSREEFYREQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAPPGQGTFPFMMPPPSMPHPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRPDFVPFPPPMPPSAQGPLPPCPIRPPFPNHQMRHPFPVPPCFPPMPPPMPCPNNPPVP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAARPGGGRPGWEHSN-KLGYLVSPPQQIRRGERSCYRSINRGRHHSERSQRTQGPS-LP 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EYDILGETGPAHNKAFDAQVIVNGQVLGKGSGRTKKQAEQSAAQFAIN-----QLTHR
                                                                       DKDKREKDKPKVKSDKTKRKSDGSATAKKDNVLKPSKGPQEKVDGDREKSPRSEPPLKKA
                                                                                                         LRDLYDKFEEELGSRQEKAKA---
                                                                                                                                            SESFLNPELLGKFRKCRGSSGIDETKTDTLFVFPSREDATPVRDEPMD--AESITFKSVS
                                                                                                                                                                                EEELLKPVWI - - - - RCTHSENY - - -
                                                                                                                                                                                                                                                                                                                         SGRSYGLSVVPEPAGCTPELPGEIIKNTDSWAP----PLEIVNHRSPSREKKRARWEEEK 369
                                                                                                                                                                                                                                                                                                                                                             K-RNVPRG-ETEREYFNRYREVPPPYDIKAYYGRSVDFRDPFEKERYREWERKYREWYEK
                                                                                                                                                                                                                                                                                                                                                                                                                                    -RRGRGKSRNY---RSRSRSHG---YHRS----RSRSPPYRRYHSRSRSPQAFRGQSPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERRSPERLKHYDDHRHRDHSHGRGERHRSLDRRERGRSPDRRRQDSRYRSDYD-RGRTPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----QYP---PGYSHHNFPPPSFNSFQNNPSSFLPSANNSSSPHFRHLPPYPLPKAPS 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151;
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                                                                                                                                                                                                                                                    -----QSSGKDKNYTSIKEKEPEETMPD------
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                                   -CSSSSDSEVFDVIAEIKRKKAH 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.9%; Score 293; DB;
23.8%; Pred. No. 1e-07;
tive 72; Mismatches
                                                                                                                                                                                                                                                                                      NREDFSPERLLPLNIRN--SPFTRGRREDYAAGQ 655
                                                                                                       -ARPPWEPPKTKLDEDLESSSESE---CES 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----YNAOOdWAddd----
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863
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                                                                                                                                                                                                                                                                                                                                                                                               -----DNRRSPSLERSYKKEYKR 313
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                                                                                                                                                                                                                                                  ---KNE---EE 403
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ribonuclease III rncS [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ribonuclease III VC2461 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: B82073
                                                                                                                                                                                                                     C; Superfamily: ribonuclease III; double-stranded RNA-binding repeat
                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-263 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, Nucleic Acids Res. 28, 4317-4331, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: A83961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 1
C; Superfamily: ribonuclease III; double-stranded RNA-binding repeat homology
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A; Residues: 1-225 <HEI>
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                                                                                                                                                                                                                                                  A; Gene: rncS
                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06208.1; A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A83961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE004316; GB:AE003852; NID:g9657034; PIDN:AAF95603.1; A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
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                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                         Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                   1084 HPLQLQEPNTDRQLIETSPVLQKLTEFEEAIGVIFTHVRLLARAFTLRTVGFNH--LTLG 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1280 DIPLYKTLQTVGPSHARTYTVAVYFKG-ERIGCGKGPSIQQAEMGAAMDALEK 1331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLESFIAALYTDKDLEYVHTFMNVCFFPRLKEFILNQDWNDPKSQLQQCCLTLRTEGKEP 1279
  HSERRRQP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLPVYTVTNIKGEAHNOEFTVACEVAGMDTPVIGKGTSRRKAEQAAAETALEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELYRRFPKVNEGDMSRMRATLVRGNTLAELGREFDLGDYLKLGPGELKSGGFRRDSILAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.8%;
1 Similarity 32.2%;
75; Conservation
                                                                                                          . Similarity 77; Conserv
                                                                                                             Conservative
-KRLTLTAKQQQMFDELLRTLNLTFANKKLLVQAFTHSSYVNEHRIQSCK 71
                                                                                                                                    30.98;
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                                                                                                                                    Score
Pred.
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Pred. No. 2.2
                                                                                                                                    282; DB 2;
No. 4.1e-08;
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H.; Dragoi, I.; Selle
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                                                                                                                                                                                                                                                                                                                                  GSPDB:G
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R;HOSKINS, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B. e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: F98012
                                                                                             ribonuclease III [imported] - Streptococcus pneumoniae C;Specles: Streptococcus pneumoniae C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #tex C;Accession: H95144
                                                                                                                                                               RESULT
H95144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ribonuclease III (EC 3.1.26.3) [imported] - Streptococcus pneumoniae (strai c;Species: Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001 C;Accession: F98012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
F98012
                              R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; on, J.D.; Umayam, L.A.; white, O.; Salzberg, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001
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C;Superfamily: ribonuclease III;
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A;Molecule type: DNA
A;Residues: 1-232 <KUR>
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 A; Authors: Loftus, B.J.; A; Title: Complete Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB: AE007317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                             VATEYLFIHFPDHHEGHLTLLRSSLVNNRTQAKVAEELGMQEYAITNDKTKRPVGLRTK- 1215 : | | : | | : | | : | | : | | : |
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                                                                                                                                                                                                                              QVNG--
                                                                                                                                                                                                                                                           RTEGKEPDIPL-YKTLQTVGPSHARTYTVAVYFKGERIGCGKGPSIQQAEMGAAMDALEK 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETSPVLQKLTEFEEAIGVIFTHVRLLARAFTLRTVGFNH---LTLGHNQRMEFLGDSIMQL
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                                                                                                                                                                                                                                                                                           TILGDAFEAFLGALLLDKDVAKVKEFIYQVMIPKVEAGEFEMITDY - - - KTHLQE - - - LL
                                                                                                                                                                                                                                                                                                                           -TLADLLESFIAALYTDKDLEYVHTFMNVCFFPRLK--EFILNQDWNDPKSQLQQCCLTL
                                                                                                                                                                                                                                                                                                                                                          LISEYLYKKYPKKPEGDLSKLRAMIVREESLAGFARDCQFDQF-IKLGKGEEKSGGRNRD 115
                                                                                                                                                                                                                                                                                                                                                                                                                       ELQTVLKNHFEIE-----FADKKLLETAFTHTSYANEHRLLKISHNERLEFLGDAVLQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
79; Conser
                                                                                                                                                                                                                         - DVAIRYQVISETGPAHDKVEDVEVLVEGKSIGQGQGRSKKLAEQEAAKNAVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
Genome Sequence of a virulent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    double-stranded RNA-binding repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIDN:AAK99930.1; PID:g15458754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 281.5;
Pred. No. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                               Eisen, J.A.;
S.L.; Lewis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nes 91;
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Venter, isolate
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                                                                                                            #text_change
                                                                                                                                            (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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J.C.; Dougherty,
of Streptococcus
                                                               Read,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae (strain
                                                                                                                                              TIGR4)
                                                               T.D.; Peterson, S.; Hei Radune, D.; Holtzapple,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                            24-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSPDB:GN00174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homology
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C; Superfamily: RING finger homology
C; Keywords: tandem repeat; zinc
E; 79-129/Domain: RING finger homology
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-948 <SAK>
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23.0%;
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A;Reference number: A95000; MUID:2135
A;Accession: H95144
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-32 <KUR>
A;Cross-references: GB:AB005672; PIDN
A;Cross-references: GB:AB005672; PIDN
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene:Sp1248
C;Superfamily: ribonuclease III; doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: A57640
R;Sakai, Y.; Saijo, M.; Coelho, K.; Kishino, T.; Niikawa, N.; Taya, Y.
Genomics 30, 98-101, 1995
A;Title: cDNA sequence and chromosomal localization of a novel human protein, A;Reference number: A57640; MUID:96129310
A;Accession: A57640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             retinoblastoma binding protein RBQ-1 - human
C;Species: Homo sapiens (man)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1108 TEFEEAIGVIFTHVRLLARAFTLRTVGFNH--LTLGHNQRMEFLGDSIMQLVATEYLFIH 1165
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                                                                                                                                                                                                                                                                                 ARPGGGRPGWEHSN-KLGYLVSPPQQIRRGERSCYRSINRGRHHSERSQRTQGPS-LPAT 377
                                                                                                                                                                                                                                                                                                                            ARPSA--PSFRPQNLRLLHPQQPPVQYQYEPPSA-----PSTTFSNSPAPNFLPPR 75
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                                                                       PPPAG---YSVPPPGFP-PAPANLSTPWVSSGVQTAHSNTIPTTQAPPLSREEFYREQRR 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GB: X85133; NID: g728590; PIDN: CAA59445.1;
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                                                                                                                                                                                                                                                                                                                                                                                    Score 276; DB 2;
Pred. No. 4.4e-07;
1; Mismatches 208
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Pred. No. 4.8
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ches 91;
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-GYSHHNFPPPSFNS 184
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A; Cross-references: EMBI
A; Experimental source: C; Genetics:
A; Map position: 4
A; Note: T9E8.80
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-Jun-1999
C;Acçession: T06091
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.
submitted to the Protein Sequence Database, April 1999
A;Reference number: Z15588
A;Accession: T06091
A;Molecule type: DNA
A;Residues: 1-760 <BEV>
CRESION: T060 SEEV>
CRESION:
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                                                -PKAPSERRSP
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                                                                                                 ----TTFSNSPAPNELPPRPDF-VPFPPPMPPSAQGPLPPCPIRPPFPNHQMRHPFPVPP
                                                                                                                                                                                                                                                                                                                                                                                                   PGRPAQRSPGQCKAFLSRP----PVNCGSFSCGRSVSP-RPPVVTPLPPPSLPSPPPPAPI 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.7%; Score 275; DB 2;
35.1%; Pred. No. 3.8e-07;
tive 15; Mismatches 96
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A;Experimental source: cultivar Columbia; BAC clone T15B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-1531 <
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                                      NHNERLEFIGDAVVEFLTSVHLYYLFPSLEEGGLATYRTAIVQNQHLAML--AKKLE--- 1017
                                                                                                                                                                                                                                                                                                    ---KKYGIVLAH--PNQPLMKLKQSHHAHNLLVDFNEEMVVKTEPKAGNVRKRKPNI----
                                                                                                                                                                                                                                                                                                                                LWKSY-VKLRHLLANSP--KVKQTDKQK---LAQREEALQKIRQK--NTMRREVTVELSS
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  FSMERLELLGDSVLKYVASCHLFLKYPDKDEGQLSRQRQSIISNSNLHRLTTSRKLQGYI 1029
                                                                                                    RLESLMLASQLREEI-DCSIDNFSISSTSI---
                                                                                                                                               HLNFGMNPDHARNSLSNCGIRQPKYGDRKVHHMHMRKKGINTLINIMSRLGQDDPTPSRI 962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGVKEIGSMVIPDSNITVSEEAASTQTMSD---PPSRNEQLPPCKKLRLDNNLLQSNGKE 569
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                                                                                                                                                                                                                                              QGFWKTGIRSDVCQHAMMLPVLTHHIRYHQCLMHLDKLIGYTFQDRCLLQLAMTHPS--H
                                                                                                                                                                                                                                                                                                                                                                                                LEELVVIAIHTGRIYSIVEAVSDSSAMSPFEVD------ASSGYATYAEYFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EECKGMIVTNPGTKPSSVRI--DQLDREQFNPDVITFPIIVHFGIRPAQLSYAGDPQYQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKYFQQFFFNGMFGKLFVGSKSQGTKREFLLQ-----TDTSSLWHPAFMFLLLPVETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----TINAGRLEHYRITVSPPTNELTDRPTVIEYDDHEYIFEGESMEAHAPLTNI 615
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      Qy
      161 PQQVNYQYPPGYSHHNFPPPSFNSFQNNPSSFLPSANNSSSPHERHLPP---YPLPKAPS
      217

      Db
      197 GDQTT-QPPPLW----LPPPPFGD-ETPPVFSLPPPLDEFPP----MPPITWLPPPDVPA
      246

      Qy
      218 ERRSPERLKH--------YDDHRHRDHSHGRGERHRSLDRREGRSPDRRRQDS
      263

      Db
      247 QTSSAEAFDQIPPLVTITEAIENPHNSHRHRD-----ENKKGLDRRNR-RVKSRRRSRS
      299

      Qy
      264 R
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Search completed: October 9, 2002, 18:26:49 Job time : 58 secs

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O9nw73 homo sapien
O9xyn5 drosophila
O9y2v9 homo sapien
O960y4 drosophila
O9y4y0 homo sapien
O01327 caenorhabdi
O9u9q8 caenorhabdi
O9u9q8 caenorhabdi
O9vay4 drosophila
O9vay4 drosophila
                          Q16630 homo sapien
Q9bw18 homo sapien
Q92ak3 listeria in
                                                                                                                                                                     Description
        P97868 mus musculu
Q9sbm1 volvox cart
                                    homo
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256	258	259	259	259.5	261	261	265	265.5	266	267	267	267	268	269	271	271.5	272.5	273	273	273.5	274.5	275	275.5	276	279.5	282	284.5	285
3.4	3. 4	ა	3.5	ω .5	3.S	ω .5	3 .5	ω .5	3 .5	3.6	3.6	3.6	3. 6	3.6	3.6	3.6	з. 6	3.6	3.6	3. 6	3.7	3.7	3.7	3.7	•	ა . 8	3.8	3.8
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Q91j64 arabidopsis	Q9esu6 mus musculu			Q9fpq6 chlamydomon	Q9c0i2 homo sapien			013849 schizosacch	Q948y7 volvox cart	0			Q931t1 staphylococ		Q95zg5 dictyosteli	Q9a105 streptococc	Q9vsh4 drosophila		Q9zw08 arabidopsis			Q9t0k5 arabidopsis	Q9vep4 drosophila	Q15290 homo sapien	Q97qg6 streptococc	5	Q96ph3 homo sapien	Q95ts9 drosophila

ALIGNMENTS

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RESULT 1
20 NRA
1D 20 NRA
AC 09NR
AC 09NR
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OS HOMO
OC BUKA
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Matches 1372; Conserva
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WU H., Xu H., Miraglia L.J., Crooke S.T.;
Wu H., Xu H., Miraglia L.J., Crooke S.T.;
"Human RNase III is a 160-kDa protein inv
processing.";
J. Biol. Chem. 275:36957-36965(2000).
EMBL; AF189011; AAF80558 1; -
InterPro; IPR001159; DS_RBD.
InterPro; IPR001159; DS_RBD.
InterPro; IPR009996; P. rich_extensn.
InterPro; IPR009999; RNase_3.
Pfam; PF00635; dsrm; 1.
Pfam; PF00635; RIBOnuclease_3; 2.
Pfam; PF00635; RRIDONUCLEASE_3; 2.
SMART; SM00358; DSRM; 1.
SMART; SM00358; DSRM; 1.
SMART; SM00359; RNASE_3_1; 2.
PROSITE; PS050137; DS_RBD; 1.
PROSITE; PS050137; RNASE_3_1; 2.
PROSITE; PS050142; RNASE_3_2; 2.
SEQUENCE 1374 AA; 159244 MW; 88810852
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Q9NRR4;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RIBONUCLEASE III.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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        Conservative
                                         99.8%;
pred. No. 0;
0; Mismatches
                                                                                                                                                                888108523912F705 CRC64;
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                                                                              DB 4;
    2;
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    Indels
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    Gaps
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Q9BSJ7

homo

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1 MMQGNTCHRMSFHPGRGCPRGRGGHGARPSAPSFRPQNLRLLHPQQPPVQYQYEPPSAPS 60

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RA Mishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Mishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Magatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Wagatsuma M., Hosoiri T., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishid S., Kawai Y., Saito K.,
RA Watanabe S., Kimura K., Murakami K., Ishid S., Kawai Y., Saito K.,
RA Watanabe S., Kimura K., Murakami K., Ishid S., Kawai Y., Saito K.,
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RA Watanabe S., Kimura K., Murakami K., Ishid S., Kawai Y., Saito K.,
RA Watanabe S., Kimura K., Murakami K., Masuho Y.,
RA Watanabe S., Kimura K., Murakamura Y., Nagahari K., Masuho Y.,
RA Watanabe S., Kimura K., Murakami K., Ishid S., Kawai Y., Saito K.,
RA Watanabe S., Kimura K., Murakawa K., Ono Y., Takiguchi S.,
RI Minomiya K., Iwayanagi T.;
RMEDO human cDNA sequencing project.";
RMEDO human cDNA sequencing proj
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Q9NW73;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 89.7 KDA PROTEIN.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606; [1]
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                                                                                                                                      EELEWQKYAEECKGMIVTNPGTKPSSVRIDQLDREQFNPDVITFFIIVHFGIRPAQLSYA 785
                                                                                                       EELEWQKYAEECKGMIVTNPGTKPSSVRIDQLDREQFNPDVITFPIIVHFGIRPAQLSYA
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99.5%;
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Pred. No. 3.5e-281;
0; Mismatches 4;
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An Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
An George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
An Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
An Handon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
An Handon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
All Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
An Hall J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baddwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beleson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
An Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
An Cherry J.M., Cawley S., Dahlke C., Davanport L.B., Davies P.,
An Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Dourbin K.J., Evangelista C.C., Perraz C., Perraz S., Fleischmann W.,
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Q9XYN5;
Q1-NOV-1999
Q1-NOV-1999
Q1-JUN-2001
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
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    Gabrielian A.E., Garg N.S.,
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Last sequence update)
Last annotation update)
        Gelbart W.M.,
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        Glasser
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Melson D.L.,
RA Mount S.M., Moly M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Syradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Syradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Walliams S.M., Woolage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woolage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong M., Zhang G., Zhao Q., Zheng L.,
RA Science 287:2185-2195(2000).
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Best Local S
Matches 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0026722; drosha.
InterPro; IPR001159; DS_RBD.
InterPro; IPR00999; RNase_3.
Pfam; PP00035; dsrm; 1.
Pfam; PP00035; dsrm; 1.
SMART; SM0036; Ribonuclease_3; 2
SMART; SM00336; DSRM; 1.
SMART; SM00535; RIBOC; 2.
PROSITE; PS00137; DS_RBD; 1.
PROSITE; PS00517; RNASE_3_1; 1.
PROSITE; PS00517; RNASE_3_1; 2.
SEQUENCE 1327 AA; 152816 MW;
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                                                                                                                             184
                                                                                                                                                             296
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 ESWVRSSPAELYYERTK---
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                               PVWIRCTHSENYYSSDPMDQVGDSTVVGTSRLRDLYDKFEEELGSRQEKAKAARPPWEPP
                                                               ETLEKTRAKPKVETERDRLLRQWCSNFC---
                                                                                  PSREKKRA--RWEEEKDR----WSDNQSSGKDKNYTSIKEKEPEETMPDKNEEEEEELLK
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                                                                                                                             AHRQAKGSQHGY---YGSAARN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                           SGSSFLYES----YKYPDRYPAYSSNYRPPSERQ------
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                                                                                                                                                                                             ---GYSSGR----
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-SENEVRGRARLQKLCTLFDEELLQRAKRVREKLPVYVPP
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MW, 2
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2963; DB 5;
Pred. No. 5.4e-202;
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                                                                                                                                                                                           -RYEQRHDQ----EHRQIQDSRYAHEPRHGHY 183
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drosha
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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STRAIN-Y, CN BW SP;

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George

Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.,

Nunco J., Pacleb J., Parragas V., Park S., Phouanenavong S., Wa

Yu C., Lewis S.E., Rubin G.M., Celniker S.;

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AY051775; ARR93199 1; -

EMBL, AY051775 ARR93199 1; -

EMBL, AY051775 ARR93199 1; -

EMBL, AY051775 ARR9319 1; -

EMBL, AY051775 ARR93199 1; -
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
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                            FEALIGAVYLEGSLEEAKQLFGRLLF-NDPDLREVWLNYPLHPLQLQEPNTDRQLIETSP
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Pred. No. 2.4e-
69; Mismatches
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2.4e-191;
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Plasmid.
NON_TER 1 1
NON_TER 380 380
SEQUENCE 380 AA; 44577 M
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Gunther M., Laithier M., Brison O.;
"A set of proteins interacting with transcription
identified in a two-hybrid screening.";
Mol. Cell. Biochem. 210:131-142(2000).
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01-DEC-2001
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01-NOV-1999
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Mammalia; Eutheria;
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Plasmid pactII.
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    EDLESSSESECESDEDSTCSSSSDSEVFDVIAEIKRKKAHPDRLHDELWYNDPGQMNDGP
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44577 MW;
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84.1%;
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Best Local Sim
Matches 364;
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O01327;
01-JUL-1997 (TrEMBLrel. C
01-OCT-2001 (TREMBLrel. 1
01-DEC-2001 (TREMBLREL. 1
F26E4.10 PROTEIN.
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Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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SMART; SM00535; RIBOC; ;
PROSITE; PS50137; DS_RBI
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EMBL; Z81070; CAB03006.3;
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Pfam; PF00636; Ribonuclease_3;
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MEDLINE=99069613; PubMed=9851916;
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InterPro; IPR000999; RNase_3.
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DELWYNDPGQMNDGPLCKCSAKARRTGIRHSIYPGEEAIKPCRPMTNNAGRLFHY--RIT
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                                                                                                             GGDESFTASDVSDDSNDS-----
                                                                                                                                             ---ENYYSSDPMDQVGDSTVVGTSRLRDLYDKFEEELGSRQEKAKAARPP--WEPPKTKL
                                                                                                                                                                              AEEAEKYMMIKAKSTTSKILQDFQTKILETVKTKRRLQADVPYIIHPCHSMKGRKTPKQK
                                                                                                                                                                                                                    EKEPEETMPDKNEEEEEELLK------
                                                                                                                                                                                                                                                        DSPRLTEKDYETNYMIDPP--VVSTHSAELIK--
                                                                                                                                                                                                                                                                                        EIIKNTDS-----WAPPLEIVNHRSPSREKKRARWEEEKDRWSDNQSSGKDKNYTSIK 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LCKCSAKARRTGIRHSIYPGEEAIKPCRPMTNNAGRLFHYRITVSPPTNFLTDRPTVIEY
                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 31.2%; Pr 64; Conservative 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282:2012-2018(1998).
81070; CAB03006.3; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS50137; DS_RBD; 1.
PS00517; RNASE_3_1; 2.
PS50142; RNASE_3_2; 2.
PS50142; RNASE_3_2; 3.
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                                     -VKDEKQTCNRRNQQRKAKRLRNFEEKERQITLLKKGIDRKKTHPNGIH
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                                                                                                                                                                                                                                                                                                                                                                                                                  19.3%; Score 1448; DB 5; 31.2%; Pred. No. 2.7e-94;
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Last annotation update)
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                                                                       -----SSSDSEVFDVIAEIKRKKAHPDRLH
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                                                                                                                                                              Q9U9Q8;
                                 RIBONUCLEASE (FRAGMENT).
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                   01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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NCBI_TaxID=6239; [1]
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PRELIMINARY;

PRT;

860 A

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Created)
Last sequence up
Last annotation

update)

update)

Rhabditida;

Rhabditoidea;

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KTLQTVGPSHARTYTVAVYFKGERIGCGKGPSIQQAEMGAAMDALEKYNFPQMAHQKRFI 1344
                                                                                                                                                                                  EFEEAIGVIFTHVRLLARAFTLRTVGFNHLTLGHNQRMEFLGDSIMQLVATEYLFIHFPD
                                           GRKYRQELKEMRWEREHQEREPDETED 1371
                                                                                                                                                                                                                                                                            ALEERLGIQFNNIRLLAKAFTRRNIPNNDLTKGHNQRLEWLGDSVLQLIVSDFLYRRFPY
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                                                                                          RVLGIEGPTNNRIFKIAVYYKGKRLASAAESNVHKAELRVAELALA--NLESMSFSK---
                                                                                                                                                                                                                                                                                                                        HHEGHLTLLRSSLVNNRTQAKVAEELGMQEYAITNDKTKRPV---GLRTKTLADLLESFI
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MKAKNNSWFQNMRRRLEQDTSD
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Matches 318;
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Pfam; PF00036; Ribonuclease_3; 2.

Pfam; PF00058; DSRM; 1.

SMART; SM00358; DSRM; 1.

SMART; SM00535; RIBOC; 2.

PROSITE; PS0137; DS_RBD; 1.

PROSITE; PS00517; RNASE_3_1; 2.

PROSITE; PS0142; RNASE_3_2; 2.
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STRAIN-CB1489 HIM-8(E1489);
MEDLINE-20179701; PubMed-10713462;
Filippov V., Solovyev V., Filippova M., Gill S.S.;
Falippov V., Solovyev V., Filippova M., Gill S.S.;
Gene 245:213-221(2000).
EMBL; Api60248; AAD45518 1; -.
InterPro; IPR001159; DS_RBD.
InterPro; IPR000199; RNASE_3.
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                                                                                                                                                                                                   HAMANCFEALIGAVYLEGSLEEAKQLFGRLLF-NDPDLREVWLNYPLHPLQLQEPNTDRQ
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{\tt TKTLADLLESFIAALYTDKDLEYVHTFMNVCFFPRLKEFILNQDWNDPKSQLQQCCLTLR}
                                                         LIETSPVLQKLTEFEEAIGVIFTHYRLLARAFTLRTYGFNHLTLGHNQRMEFLGDSIMQL
                                                                                                                                                                              HALANAF EAVMAAIYLDGGLAPCDVIF SKAMYGHQPVLKEKWDHINEHELKREDPQGDRD
                                                                                                                                                                                                                                                    LIVSHHLYFMLTHHFEGGLATYRTALVQNRNLATLAKNCRIDEMLQYSHGADLINVAEFK
                                                                                                                                                                                                                                                                       CGYRR-KYGAEDKR----EKKRVAGIMSLFNIMKGTSGGEP----ILHNERLEYLGDAVVE
                                                                                                                                                                                                                                                                                                                                           CGIRQPKYG--DRKVHHMHMRKKGINTLINIMSRLGQDDPTPSRINHNERLEFLGDAVVE
                                                                                                                                                                                                                                                                                                                                                                                              VVMTTLACHHIRYNFSLDVFEEVIEYKFNDRRVIELALMHSSFKSHYGTPIDHVKNMITN
                                                                                                                                                                                                                                                                                                                                                                                                                      AMMLPVLTHHIRYHQCLMHLDKLIGYTFQDRCLLQLAMTHPSHHLNFGMNPDHARNSLSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRHLLANSPKVKQTDKQKLAQREEALQKIRQKNTMRREVTVELSSQGFWKTGIRSDVCQH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIVTNPGTKPSSVRIDQLDREQFNPDVITFPIIVHFGIRPAQLSYAGDPQYQKLMKSYVK
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                                    IVSDFLYRRFPYHHEGHMSLLRTSLVSNQTQAVVCDDLGFTEFVI-----KAPYKTPELK
                                                                                                          LSFITPTLSTFHALEERLGIQFNNIRLLAKAFTRRNIPNNDLTKGHNQRLEWLGDSVLQL
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36.2%;
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3; Mismatches
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Pred. No. 3
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A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninol P., de Bonaldo M.F.,
A Blake J., Boffelli D., Bojunga N., Carninol P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Gustincich S., Hill D., Mashima J., Mazzarelli J., Mombaerts P.,
A Gustincich S., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Scohenbach C., Seya T., Shibata Y., Storch K.-F.,
A Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Bayashira-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local S
Matches 131
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Q9CTG2;
Q1-JUN-2001
Q1-JUN-2001
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Hayashizaki Y.;
"Functional annotation of a full-length
Nature 409:685-690(2001).
EMBL; AK003651; BABZ2917.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TIEMBLrel. 17, Created)
01-JUN-2001 (TIEMBLrel. 17, Last sequence update)
01-JUN-2001 (TIEMBLrel. 17, Last annotation update)
1110013A17RIK PROTEIN (FRAGMENT).
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                                    1361
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AK003651; Ba
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121
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                   HQEREPDETEDIKK
                                                                     AVYFKGERIGCGKGPSIQQAEMGAAMDALEKYNFPQMAHQKRFIERKYRQELKEMRWERE
                                                                                                          AVYFKGERIGCGKGPSIQQAEMGAAMDALEKYNFPQMAHQKRFIGRKYRQELKEMRWERE 1360
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                                                                                                                                                                                                                                                                                              15883 MW;
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                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA collection.";
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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.I.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktarcoglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Bortkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Caddeu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson K.A.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Wang Z.-Y., Wassarman D.A., Weinsche R.M., Skupski M.P., Smith T.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinschot G.M., Venter E., Shao Q., Zheng L.,
RA Zheng X.H., Zhong F. N., Zhong W., Zhang G., Zhao Q., Zheng L.,
RA Cheng S., Yao Q.A., Pan S., Pollard J., Wang S., Yao Q.A.,
RA Zheng X.H., Zhong F. N., Zhong W., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong W., Rubin G.M., Venter J.C.,
RA Zhao Q., Zheng L.,
                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).

EMBL, AE003763; AAF56763.1; -.
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0039560; CG5514.
InterPro; IPR002965; P_rich_extensn.
PRIWIS; PRO1217; PRICHEXTENSN.
SEQUENCE 1151 AA; 125450 MW; AF8
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01-JUN-2001
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PPMPPSAQGPLPPCP--IRPPEPNHQMRHPFPVPPCFPPMPPPMPCPN--NPPVPGAP-- 136
                                                                                                                RPASPKVEPP-----
                                                                                                                                                                              RPSAPSFRPQNLRLLHPQQPPVQYQYEPPSAPSTTFSNSPAPNFL----PPRPDFVPFP
                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                       4.5%;
22.5%;
                                                                                                            PPAPPGVESPPGPQPPASPRFDPPPPHTIEPPPPPAPPTLVPPP 415
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Last sequence up
                                                                                                                                                                                                                                               Score 340; DB 5;
Pred. No. 2.1e-15;
3; Mismatches 280
                                                                                                                                                                                                                                                                                                                                                                                         AF8330378C58C1D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1151
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                                                                           VTHF-EENTDE-
                                                                                                         TIHFIEEMMPENFCVKGLELFSLFLFRDILELYDW-----NLKGPLFED 671
                                                                                                                                                                                                                              RKKAHPDRLHDELWYNDPGQMNDGPLCKCSAKARRTGIRHSIYPGEEAIKPCRPMTNNAG
                                                                                                                                      -----PQDADKPATPVPISNEQSDEFSADF
                                                                                                                                                                   RLFHYRITVSPPTNFLTDRPTVIEYDDHEYIFEGFSMFAHAPLTNIPLC--KVIRFNIDY
                                                                                                                                                                                                                                                             QSHDRAESSKHEPEDIDGKEADNQPEKTELEARQDE-CASQNEVPTVEPQTLADSVPDLP
                                                                                                                                                                                                                                                                                         QEKAKAARPPWEPPKTKLDEDLESSSESECESDEDSTCSSSSD-----SEVFDVIAEIK
                                                                                                                                                                                                                                                                                                                         QPEDSAATMKSDAPVENANGTNGNSNGSTNGACDNVSGVVIVSDILQQSTSSFVELTAGS
                                                                                                                                                                                                                                                                                                                                                      EEEEE----LLKPVWIRCTHSENYYSSDPMDQVGDS---TVVGTSRLRDLYDKFEEELGSR
                                                                                                                                                                                                                                                                                                                                                                                     KDHDRGRDRDRNKSNTSGSAENKAIHDDHSESKEKYKQRRGSDSNDEGKPPSSGGPAKNS
                                                                                                                                                                                                                                                                                                                                                                                                                  WEEEKDRWSD---NQSSGKDKN-----YTSIKE-----KEPEETMPDKNE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRYRSDYDRGR-TPSRHRSYERSRERERERHRHRDNRRSPSLER-----SYKK 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRHLPPYPLPKAPSERRSPERLKHYDDHRHRDHSHGRGERHRSLDR-RERGRSPDRRRQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                HKSSSSSRSERDKG-----KEKDKEREKDSQSRS-----HHSSSSSSSSSRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----EYKRSGRSYGLSVVPEPAGCTPELPGEIIKNTDSWAPPLEIVNHRSPSREKKRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSSSSKHSSSNSSSSKHKSSSSKNDKSSSSSSSSRSNRESSSSKRSGTTSSSRHESSSHKK
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -KSHSKSRDKEKEKDRRHHRHSDDKH----RRRSTDRDRDRSRDKSHSKHS
                                                                                                                                                                                                   -----KVETNVEEN--KSEEESKP-----
PRT;
                                                                           FRTRLQLINQLIEDRKNLLNRLSED
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Query Match
                                                                        SEQUENCE FROM N.A.
Fleischhauer K.L.;
Submitted (JUN-1995) to the
EMBL; X67337; CAA47752.1;
EMBL; X67336; CAA47751.1;
                    InterPro; IPR000504; RRM.

pfam; pF00076; rrm; 1.

SMART; SM00360; RRM; 1.

pROSITE; pS50102; RRW; 1.

SEQUENCE 551 AA; 59208 MW;
                                                                                                                                                                                                                           Q16630;
01-NOV-1996
                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                  HPBRII-4 MRNA.
HPBRII-4 OR HPBRII-7.
                                                                                                                                                                                                        01-NOV-1996
01-JUN-2001
                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                        (TrEMBLrel.
                                                                                                                                                   Chordata;
Primates;
                                                                                                                                                                                                      01, Created)
01, Last sequence update)
17, Last annotation update)
                                                                                               the EMBL/GenBank/DDBJ databases
                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                      407CB941B456A966 CRC64;
 316;
 DB
 4
 Length 551;
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Matches

Best

Local Similarity

28.0%;

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RESULT

OPENIES

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                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00076; rrm; 1.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ
EMBL; BC000714; AAH00714.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT.
Homo sapiens (Human).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN 2001 (TrembLrel. 17, Created)
01-JUN-2001 (TrembLrel. 17, Last sequence update)
01-DEC-2001 (TrembLrel. 19, Last annotation update)
SIMILAR TO CLEAVAGE AND POLYADENYLATION SPECIFIC FACTOR 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9BW18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002965; P_rich_extensn.
InterPro; IPR000504; RRM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                            PRGRGGHGARPSAPSFRPONLRLLHPQQP--PVQYQYEPPSAPSTTFSN---SPAPNFL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AP-HVN----PAF----FPPPT-----NSGMPTSDSRGPPPTDPYGRPPPYDRGDYG
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                          HQMRHPFPV-
                                                                          TRIPWHMGHSIEEIPIFGLKAGQTPPRP----PLGPPGPPGPPPPGQVLPPPLAGPPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DRHDDYYRERSRERERHRDRD--RDRDRERDREREYR 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSKVSADDRCKVLISSLQDCLHGIESKSYGSGSRRERSRERDHSR--SREKSRRHKSRSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MPQQVNYQYPPGYSHHNFPPPSFNSFQNNPSSFLPSANNSSSP---HFRHLPPY-----
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                                                                                                                                                                               PQGGRGRGRFPGAV - - - PGGDRFPGPAGPGGP - - - - -
                                                                                                                                                                                                                                                                                 116;
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                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                 588 AA;
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                                                                                                                                                                                                                                                                                                    4.18;
                                                                                                                                                                                                                                                                                                                                                                                 63470 MW; 1F2B7051251A7E52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----HG-RGERHRSLDRRERGRSPDRRRQDSRYRSDYDRGRTP
=
                          PPC - - FPPMPPPMPCPNNPPVPGAPPGQ -
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                                                                                                                       -PPRPDFVPFPPPMPPSAQGPLPPCPIRPP----FPN 104
                                                                                                                                                                                                                                                                            Score 306.5; DB Pred. No. 2e-13; 0; Mismatches 1
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A Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

A Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

A Domann K.-D., Fishi H., Garcia-del Portillo F., Garrido P.,

A Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

A Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

A Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

A Nordsiak G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

A Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

"Comparative genomics of Listeria species.";

Science 294:849-852(2001).

BEBL; AL596170; CAC97149.1; -.
                                                                                                                                                                                           Query Match
Best Local
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Q92AK3;
Q1-DEC-2001
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Bacteria; Firmicutes;
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01-DEC-2001
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IGALYLDNGIDKVVKFLERVIFPKIDAGAYLQTVDY---KTQLQEIV----
                           IAALYTDKDLEYVHTFMNVCFFPRLK--EFILNQDWNDPKSQLQQCCLTLRTEGKEPDIP 1283
                                                         PDMAEGHMTKMRAAIVCEPSLVEFAEAVHFSKY-VRLGKGEEKAGGRTRPALLADVFESF
                                                                        PDHHEGHLTLLRSSLVNNRTQAKVAEELGMQEYAITNDKTKRPVGLRTK--TLADLLESF 1224
                                                                                                                  ELQESVGFDFQNVELLQQAFTHSSYVNEHRRENVKDNERLEFLGDAVLELTVSDYLFNKY 65
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Last annotation update)
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                                                                                                                                                                                        Score 300; DB 16;
Pred. No. 1.5e-13;
                                                                                                                                                                           Pred. No. 1.5
3; Mismatches
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"PACT: cloning and characterization of
that interacts with Rb.";
Oncogene 14:145-155(1997).
-!- FUNCTION: BINDS TO RBI THROUGH THE
WITH HURNPA. ALSO BINDS TO P53. MAN
AND DIFFERENTIATION.
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                                                                                                                                                                                                                 Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
PROSITE; PS00518; ZINC_FINGER_C3HC4; FALSE_NEG.
Zinc-finger; Metal-binding; DNA-binding; Nuclear
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MEDLINE=97163396;
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witte M.M., Scott R.E.;
                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                            EMBL; U83913; AAC72432.1; -. EMBL; U28789; AAB49620.1; -. MGD; MGI:894835; Rbbp6. InterPro; IPR001841; Znf_ring
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                                                                                                                                                                                  ZN_FING
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                                                                                                                                                                                                                                                                                                                                                                                             ISOFORM 2; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN TESTIS.
MODERATE LEVELS FOUND IN HEART, LUNG, LIVER AND SKELETAL MUSCLE.
WERY LOW LEVELS DETECTED IN KIDNEY, BRAIN AND SPLEEN. ALSO
EXPRESSED IN GROWING UNDIFFERENTIATED MESENCHYMAL STEM CELLS BUT
NOT DURING THE TERMINAL DIFFERENTIATION PHASE.
SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
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ALTERNATIVE PRODUCTS: TWO ISOFORMS; ISOFORM 1 (SHOWN HERE)
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                                                                                                                                                         TKTDTLFVLPSRDDATPVRDEPMD--AESITFKSVSDKDKREKDNPKVKSDKTKRKSDGS
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Q9SBM1
ID Q9SBM
AC Q9SBM
AC Q9SBM
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OC Eukar
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                                                                                              Query Match
Best Local S
Matches 76
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                                                                                                                                                                                       Signal.
SIGNAL
                                                                                                                                                                                                                                                                           1239
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                                                                                                                                                         SEQUENCE
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InterPro; IPR003882; P_iich_extensn.
PRIMTS; PR01217; PRICHEXTENSN.
PRINTS; PR01218; PSTLEXTENSIN.
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20044763; PubMed=10574980;
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-HK10
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Volvocaceae; Volvox.
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85 MPPSAQGPLPPCPIRPPFPNHQMRHPFPVPPCFPPMPPPMPCPNNPPVPGAPPGQGTFPF 144
                                                                                                            Local Similarity
                                                           APSFRPQNLRLLHPQQPPVQYQYEPPSA--PSTTFSNSPAPNFLPPRPDF----VPFPPP 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYGKPSSIIKNVTTKPSAT-AKYTEKESEQPE------KLQKL 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C---VKGLELFSLFLFRDILELYDWNLKGPLFEDSPPCCPRFHFMPRFVRFLPDGGKEVL 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPRKAHSKSAKEHQEAKPAKDEKVKKDCSKDIKSEKPASK-DEKAKKPEKNKLLDSKGEK 947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WK--SYVKLRHLL-----ANSPKVKQTDKQKLAQREEALQKIRQKNTMRREVTVE-LSS 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSEEKTDTKRTVIKTMEEYNNDNTAPAEDVIIMIQVPQSKWDKDDFESEEEDVKTTQPIQ 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMHQILLYLLRCSKAL-------VPEEEIANMLQ-----WEELEWQKYAEECK-----
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                              APARKPP-----PRRSPVVALVETPAAPPPGSPPPGTPPPGVPPPTPSGPEHPPPPPPP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GMIVTNPGTKPSSVRIDQLDREQFNPDVITFPIIVHFGIRPAQLSYAGDPQYQKL 793
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                                                                                                                                                         409 AA;
                                                                                              Conservative
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18
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                                                                                                                                                                          409
                                                                                                                                                         41547 MW;
                                                                                          3.8%; Score 285; DB 10; 38.4%; Pred. No. 4.1e-12; tive 11; Mismatches 79;
                                                                                                                                                        HYDROXYPROLINE-RICH GLYCOPROTEIN DZ-HRGP; CD0749C6AF02BD74 CRC64;
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                                                                                                                       Length 409;
                                                                                            Indels
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PPSPPPSPPPSPPPPP
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                        MMPPPSMPHPPPPPVMPQQVNYQYPPGYSHHNFPPPSFNSFQNNPSSFLPSANNSSSPHF
190
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